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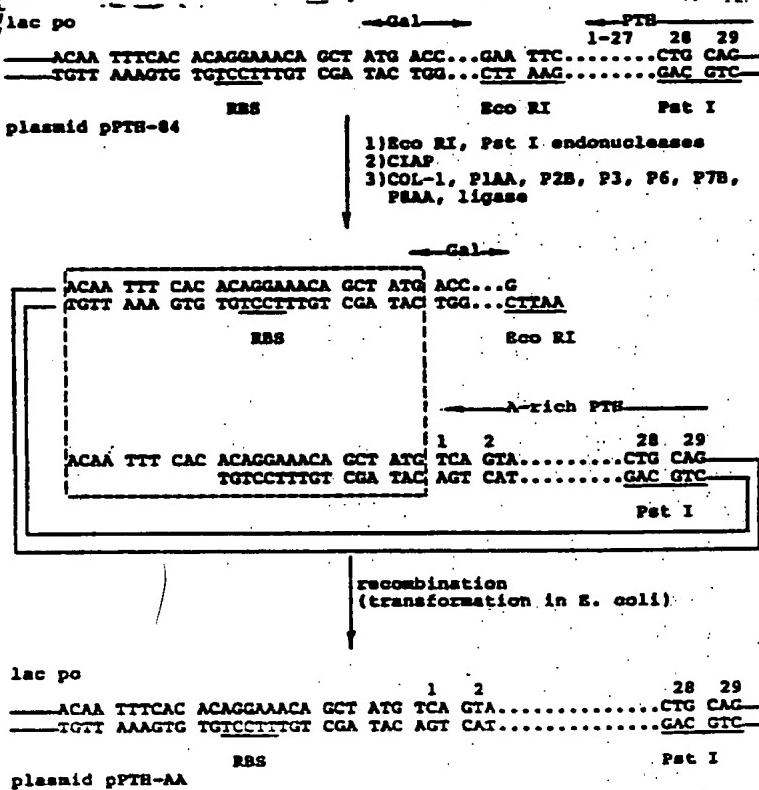
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(54) Title: SYNTHESIS OF MATURE HUMAN PARATHYROID HORMONE

(57) Abstract

A nucleotide coding sequence for human parathyroid hormone has been synthesized, which sequence results in a substantially higher yield of mature PTH than hitherto could be obtained. This is achieved by providing a synthesized nucleotide sequence coding for mature human PTH or a biologically active analog, wherein the amino terminal coding sequence is adenine-rich. A sequence wherein the degenerate codons for some or all of amino acids 1 through 5 are adenine-rich is preferred.



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SYNTHESIS OF MATURE HUMAN PARATHYROID HORMONE

Human parathyroid hormone (PTH) is a polypeptide of 84 amino acid residues. Its amino acid sequence has 5 been known since the 1970's (Habener 1978).

Parathyroid hormone is known to be a major regulator of blood calcium concentration (Keutmann 1974 and Keutmann 1978). Moderate doses of the hormone are known to increase bone mass (Kalu 1970). Limited clinical trials 10 have demonstrated that the amino-terminal portion of the molecule is active in producing the characteristic effects of parathyroid hormone on bone (Habener 1978 and Reeve 1980).

PTH has, accordingly, been demonstrated as having 15 a useful therapeutic effect in respect of bone disorders including osteoporosis and other conditions relating to bone repair and bone loss.

A 38 amino acid PTH fragment and the chemical means for its synthesis is described by R.D. Hesch in 20 German Offenlegungsschrift 3,243,258.

A synthetic fragment consisting of the first 34 amino acids of human parathyroid hormone (hPTH-(1-34)) has demonstrated a catabolic effect in patients afflicted by osteoporosis (Reeve 1980). Bone formation rates increased 25 markedly following long term daily subcutaneous injections in osteoporetic patients of a preparation including human PTH-(1-34) (Reeve 1980 and Reeve 1981). It is believed that parathyroid hormone stimulates bone formation indirectly, by stimulating the local production and release 30 of a growth factor or factors within the bone. It is further believed that parathyroid hormone also stimulates osteoclasts to secrete proteases and other factors which enable osteoclasts to resorb bone, stimulate the proliferation of osteoclast precursors in bone, and increase the 35 number of osteoclasts in bone.

While the synthetic fragment PTH-(1-34) has exhibited most of the biological activity, recent

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experiments indicated discrete binding sites for the carboxyl terminal (53-84) region in renal and skeletal tissue (Murray 1989), to provide structural elements required for optimal presentation of the biologically active domain of PTH to the receptor (Born 1988).
5 Therefore mature (i.e. intact) PTH-(1-84) may have an advantage over the shorter synthetic PTH-(1-34). Synthesis of mature PTH-(1-84) would enable such studies.

The chemical synthesis of PTH and PTH fragments
10 is expensive and laborious. Recombinant DNA techniques provide an alternative approach. The cDNA of human preproparathyroid hormone (prepro PTH), a precursor of PTH has been cloned and sequenced (Hendy 1981). PTH was produced and secreted at 0.0015 mg/litre by inserting the
15 precursor prepro PTH cDNA into a recombinant retrovirus for infection of rat pituitary cells (Hellerman 1984). However this yield from mammalian pituitary cells was too low to be useful.

Prepro PTH cDNA has also been cloned in
20 Escherichia coli (Born 1987b and Born 1988). However instead of mature PTH, only shorter fragments particularly PTH-(3-84) and PTH-(8-84) were produced intracellularly. Efforts to produce or secrete mature PTH using prepro PTH cDNA in yeast has also failed (Born 1987a).

25 Direct expression of cDNA encoding mature PTH has been described under the control of various promoters (lac, trp or tac). E. coli transformed with mature PTH cDNA was induced to produce PTH intracellularly at a reported yield of about 0.2 mg/litre (Breyel 1984). Subsequent related
30 studies resulted in reports of an improved production yield of PTH by E. coli to 0.47 mg/litre, through further gene manipulation (Morelle 1988). Other laboratories including our own have obtained the same order of efficiency of production of PTH by E. coli (Rabbani 1988). However on
35 analysis of the PTH mixture, we typically isolated shorter fragments such as PTH-(8-84) (Rabbani 1988). The yield of mature (i.e. intact) PTH may accordingly be even lower than

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predicted by Breyel and Morelle. Efforts to improve these relatively low yields in E. coli have been unsuccessful, and it was postulated that this was due at least in part to instability of PTH and related messenger RNA

5 intracellularly (Morelle 1988 and Wingender 1989).

For the estimation of PTH production yield, the most commonly used method has been the Mid-Molecule PTH Radioimmunoassay, which uses an antibody specific to the narrow mid-section (44-68) of the PTH molecule. Obviously 10 such antibody (and therefore such assay) cannot distinguish the intact PTH molecule from any degraded short fragments still maintaining the (44-68) sequence. This PTH radioimmunoassay (PTH RIA) is accordingly capable of inflating the estimation of intact PTH. Data from the Mid-Molecule PTH RIA represents merely an estimation of an 15 immunoreactive component in the PTH mixture, but not necessarily of biologically active, intact PTH. Such shortcomings show the inadequacy of relying solely on PTH RIA for estimation and characterization of intact PTH, as 20 is the case in some reports (Breyel and Morelle).

This detection inadequacy is evident in the expression of cDNA for mature PTH in yeast with the yeast alpha-factor prepro sequence used as the secretory signal (Gabrielsen 1988; Gautvik 1989a). Production of an 25 immunoreactive PTH substance was estimated by these researchers as being from 1-7 mg/litre. In the PTH mixture, in addition to intact mature PTH (comprising less than 25% of the immunoreactive mixture), several fragments of PTH were also isolated, being results of in vivo 30 cleavage at amino acid positions 27, 35 and 45 in the PTH sequence (Gabrielsen 1988). This is consistent with our own unpublished studies involving expression and secretion 35 of alpha-factor PTH fusion protein in yeast. Our initial Mid-molecule PTH RIA detected a relatively high level of PTH, namely 20mg/litre, however, upon measuring by the more accurate Allegro PTH Radioimmunoassay (Nichols Institute

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Diagnostics, San Juan Capistrano, Ca.), we discovered that less than 1% of the product could be classified as potentially intact. The Allegro PTH RIA is a two-site immunoradiometric assay simultaneously binding 2 different 5 antibodies, one in N-terminal PTH-(1-34) sequence, the other in the mid to C-terminal PTH-(39-84) sequence. This assay accordingly provides a more accurate assessment of the yield of biologically active intact PTH than does a Mid-molecule assay used by, for example, Gabrielsen, which merely identifies a single mid-molecule binding site and 10 therefore could conceivably be measuring an immunoreactive PTH mixture containing PTH fragments in addition to intact PTH.

In another study, cDNA encoding mature PTH was 15 cloned in E. coli, and PTH is reported as having been produced as a secreted polypeptide at a yield up to 10 mg/litre (estimated by Mid-molecule PTH RIA using a protein A leader sequence and promotor (Gautvik 1989a). However 20 intact PTH constituted less than one-third of the immunoreactive PTH mixture (Gautvik 1989b). Unpublished work in our laboratory using a secretory system of E. coli 25 for production of PTH was able to achieve a yield of 15 mg/litre of PTH (when measured by Mid-molecule PTH RIA), but only at most 10% of this product mixture comprised potentially intact PTH (when measured by Allegro PTH RIA).

Because of the recognized problem of protein instability, it has also been attempted to express PTH as a fusion protein with beta-galactosidase which results in a measured yield of 35-50 mg of PTH/litre (Wingender 1989). 30 The fusion site Asp-Pro permits a chemical cleavage by acid hydrolysis to yield an 85 amino acid-proline-PTH analog. However, there is no established method for the removal of the extra proline in order to generate authentic intact PTH.

35 In the result, all known recombinant means of expressing mature human PTH have resulted in low production yields, and prevalence of PTH fragments or analogs, many of which are not biologically active. Where the expression

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vehicle is E. coli, and PTH is produced as a secreted polypeptide, there is an adverse effect on yield due to proteolytic degradation during secretion.

5 We have now synthesized a nucleotide coding sequence for human parathyroid hormone, which sequence results in a substantially higher yield of mature PTH than hitherto could be obtained. The nucleotide sequence encoding the amino-terminal end of PTH, particularly amino acids 1 through 28, especially amino acids 1 through 5, have been synthesized for optimal expression of intact human PTH. We have established the conditions for optimizing the expression of our synthesized human PTH gene.

15 It is a feature of this invention to provide a means for the synthesis of mature human PTH including biologically active analogs, which avoid the low yields and product instability problems of the prior art methods.

20 It is another feature of this invention to provide a synthesized nucleotide coding sequence, which codes for mature human PTH including biologically active analogs.

25 It is another feature of this invention to provide an expression system for intracellular production of mature human PTH and biologically active analogs.

30 It is another feature of this invention to provide a method of expressing and recovering mature human PTH and biologically active analogs.

35 It is another feature of this invention to provide transformed cells containing synthetic nucleotide sequences encoding mature human PTH and biologically active analogs.

The invention achieves these features by providing a synthesized nucleotide sequence coding for mature human PTH or a biologically active analog, wherein the amino terminal coding sequence is adenine-rich. A sequence wherein the degenerate codons for at least some of

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amino acids 1 through 5 are adenine-rich is preferred. A sequence wherein the degenerate codon for amino acid 1 is guanine-rich and the degenerate codons for amino acids 2 and 3 are adenine-rich, and a sequence wherein the 5 degenerate codons for amino acids 1 through 3 are adenine-rich are particularly preferred. It is also preferred to select degenerate codons for the amino terminal coding sequence so as to avoid constituting a potential ribosome-binding site. Also preferred is any of 10 the above sequences modified to code for a mutant PTH wherein aspartic acid is substituted for the usual amino acid at position 38.

15 In drawings illustrating embodiments of the invention,

Figure 1 is a schematic diagram summarizing the synthesized nucleotide sequence encoding mature human PTH contained in plasmid pPTH-84;

20 Figure 2 is a schematic diagram showing the two step synthesis of plasmid pPTH-84;

Figure 3 summarizes the synthesized nucleotide sequence encoding PTH-(1-28) in adenine-rich plasmid pPTH-AA;

25 Figure 4 is a schematic diagram summarizing the construction of plasmid pPTH-AA;

Figure 5 summarizes the synthesis of adenine-rich plasmid pPTH-AA;

30 Figure 6 summarizes the synthesized nucleotide sequence encoding PTH-(29-84) constructed with degenerate codons in the usage frequency favoured by E. coli;

Figure 7 is a schematic diagram summarizing the construction of plasmid pPTH-AA-Eco;

35 Figure 8 is a depiction of the gel electrophoretic analysis of product expressed by various synthesized PTH plasmids;

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Figure 9 is a depiction of immunological blot identification of intact PTH and short analog PTH-(8-84) produced in E. coli;

5 Figure 10 is a depiction of immunological blot identification of intact PTH and short analog PTH-(8-84) produced from plasmids containing human-favoured codons at the amino terminal of the PTH gene;

10 Figure 11 is HPLC chromatograms illustrating the purification of recombinant PTH;

Figure 12 is mass spectra of purified recombinant PTH-(1-84) and PTH-(8-84); and

15 Figure 13 is a graph of an adenylate cyclase assay of recombinant intact PTH.

Taking advantage of the known degenerate codons for amino acids, we synthesized various plasmids each containing a PTH-coding nucleotide sequence rich in adenine, particularly at codons relating to amino acids 1 through 28, and especially at one or more of the codons 20 relating to amino acids 1 through 5. We discovered that an adenine-rich amino-terminal coding sequence resulted in the selective production of mature human PTH at a substantially higher yield. In particular, when amino acids 1 through 5 of PTH were coded in an adenine-rich fashion, yields of 25 mature PTH were increased by a factor at least of 10 over that obtained using normal human PTH codons for amino acids 1 through 5.

We have also discovered that fragments of PTH, such as PTH-(8-84) become the major component of the PTH product whenever the codon ATG encoding the amino acid methionine at position eight of PTH, functions as an internal start codon. Normally, codon ATG immediately upstream of the PTH coding sequence codes for formyl methionine, and should serve as a starting codon for PTH, 35 with the formyl methionine being excised in the normal course of events once the PTH has been synthesized. However, with the utilization of any guanine-rich

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degenerate codons especially at positions 3 and/or 4, ATG at position eight is efficiently misread as though it were the start codon, thus bypassing the upstream ATG, and causes mainly synthesis of PTH-(8-84), thereby greatly
5 reducing the total yield of intact PTH. The PTH fragment produced is (8-84) rather than (9-84) because methionine at position eight is not successfully removed from its neighbouring amino acid, histidine, at position nine, histidine having (compared with serine at position one) a
10 relatively large radius of gyration which prevents the usual methionine aminopeptidase system from operating.
(Sherman 1985).

15 The following examples provide a more detailed description of the invention.

PRELIMINARY EXAMPLE: Preparation of plasmids pPTH-84 and pPTH-84c containing synthesized nucleotide sequence.

We earlier synthesized a nucleotide sequence
20 encoding the known amino acid structure for human PTH and synthesized plasmids containing our synthesized nucleotide sequence. (Sung 1986a and Rabbani 1988). These procedures are set out below. The synthesized nucleotide sequence encoding human PTH in plasmid pPTH-84 is set out in Figure
25 1. The nucleotide sequence generally utilizes degenerate codons in the frequency favoured by yeast, for the amino acids encoded.

Materials and methods

Enzymes and plasmid pUC8 were purchased from
30 Bethesda Research Laboratories and Boehringer Mannheim.
Escherichia coli K-12 strain JM103 ($\Delta(\text{lac pro})$, thi,
str A, sup E, end A, sbc B, hsd R, F tra D36, pro AB,
lac I^Q, ZΔM15) was used.

35 Synthesis of oligonucleotides

The sixteen deoxyribooligonucleotides PI-PXVI (Figure 2), encoding PTH with the frequently used yeast

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codons, were synthesized by DNA synthesizer model 380A (Applied Biosystem) and purified on 12% polyacrylamide gel containing 7 M urea.

5 Construction of plasmid pPTH-34 and pPTH-40

Each of the eight oligonucleotides PI-PVIII

(1.3 pmol, 1 μ L) (A in Figure 2) was phosphorylated in a mixture containing 0.4 μ L of 10 X kinase buffer, 0.4 μ L of 1 mM ATP, 0.4 μ L of T4 DNA kinase, and 3 μ L of water. Phosphorylation reaction was carried out for 1 h at 37°C.

10 The solutions were then combined and heated to 70°C for 10 min. After being cooled slowly to room temperature, the combined solutions were added to a mixture of 3.5 μ L of 10 X ligase buffer, 3.5 μ L of 4 mM ATP, 0.1 pmol of EcoRI-
15 HindIII linearized plasmid pUC8, and 3.5 μ L of T4 DNA ligase and incubated at 12°C for 20 h. Aliquots of the ligation mixture were used to transform E. coli JM103 in YT plate containing ampicillin. Transformants were selected by the loss of β -galactosidase activity (X-Gal and
20 isopropylthiogalactoside) for hybridization analysis.

Labelling of the hybridization probe

Oligonucleotides PI-PV (10 pmol, 1 μ L) were phosphorylated individually with [32 P]ATP (10 pmol, 3 μ L) in 1 μ L of T4 DNA kinase, 1 μ L of 10 X kinase buffer, and 4 μ L of water at 37°C for 1 h.

Screening of plasmid containing the PTH-(1-40) gene

Colonies were chosen and grown on 10 copies of nitrocellulose filters on YT plates with ampicillin overnight. They were then denatured with 0.5 N NaOH-1.5 M NaCl (10 min) and neutralized with 0.5 N Tris-HCl (pH 7.0) - 1.5 M NaCl (10 min). After 2 h at 80°C in a vacuum oven, the filters were washed with 6 X SSC - 0.05% Triton X-100 for 30 min. Cell debris was scraped off completely. After another 30 min in fresh solution, the duplicate filters were transferred individually into separate

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mixtures of 6 x SSC - 1% dextran sulphate - 0.05% Triton X-100 - 1 Denhardt's hybridization fluid. Individually appropriate ^{32}P -labelled probes were added to a pair of filters. After 16h at 45°C, filters were washed twice with 5 6 x SSC - 0.05% Triton X-100 at room temperature for 5 min and then at 45°C for 45 min, and were analyzed by autoradiography. Filters were washed again at 75°C for 45 min, followed by autoradiographic analysis.

10 Preparation of plasmids pPTH-34 and pPTH-40 via sub-cloning

Transformants positively identified by either probe PIV or PV were cultured for the minipreparation of plasmids to transform the E. coli JM103 once again. Colony 15 hybridization with ^{32}P -labelled probes PVI and PV were used to identify plasmid clones, pPTH-40 encoding the regular amino acid sequence from position 1 to 40 of PTH and pPTH-34 which has termination at oligonucleotide triplet position 35. The PTH-coding region was sequenced with the 20 dideoxytermination method.

Construction of plasmids pPTH-84 and pPTH-87

Plasmid pPTH-40 was linearized by incubating with restriction enzymes SstI and HindIII. The phosphorylation 25 of the other eight oligonucleotides PIX-PXVI (B in Figure 2) and their ligation into the linearized plasmid pPTH-40 were similar to the construction of the latter plasmid. Transformed JM103, with plasmids bearing the whole PTH gene, was identified by hybridization with ^{32}P -labelled 30 probes PIX-PXIII. Isolated plasmids were similarly subcloned and analyzed by DNA sequencing with the "dideoxy" method.

Results

35 Eight synthetic oligonucleotides PI-PVIII, constituting the first half (oligonucleotide triplet positions 1-40) of the PTH gene (A in Figure 2), were

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phosphorylated and ligated directly into linearized plasmid pUC8 in a single operation without any intermediate purification of gene assembly.

Base mismatch was designed at nucleotide triplet position 35, between complementary oligonucleotides PIV (GTT, valine) and PV (TTA, complementary triplet of the termination codon) (A in Figure 2). Transformation in JM103 by recombinant plasmid-bearing fragments PI-PVIII subsequently yielded two plasmids: pPTH-40 coding for a legitimate half of PTH (PTH 1-40) with the termination codon in the HindIII site and pPTH-34 encoding a shorter fragment (PTH(1-34)) because of the predetermined termination codon at triplet position 35.

Hybridization with ^{32}P -labelled PI-PV at 45°C identified transformants bearing the general PTH-coding sequence. At an elevated temperature of 75°C, both PIV and PV were capable of distinguishing between colonies predominant with plasmids pPTH-40, and pPTH-34, respectively. DNA sequencing of the two plasmids confirmed that pPTH-40 had a valine codon (complementary triplet AAC) at position 35 and pPTH-34 had termination (complementary triplet TTA) at the same site.

Plasmid pPTH-40 was then digested with restriction endonucleases SstI and HindIII. Synthesis of the whole PTH gene was then completed via phosphorylation and ligation of another eight synthetic oligonucleotides, PIX-PXVI constituting the rest of the PTH gene (positions 39-84) (B in Figure 2), into the linearized plasmid pPTH-40.

Base mismatch at oligonucleotides triplet position 85 of the two complementary fragments PXII (TAA, termination codon) and PXIII (ACA, complementary triplet of cysteine) resulted in the formation of two different PTH gene-bearing plasmids, pPTH-84 and pPTH-87. These bore the proper coding sequence with termination at position 85 or a cysteine codon (TGT) at the same position, respectively.

Bacterial transformants with these plasmids were identified by hybridization with ^{32}P -labelled fragments

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PIX-PXIII as before. Plasmids were prepared from these transformants for subcloning. Dideoxy DNA sequencing of the subcloned plasmids showed two types of PTH-coding plasmids pPTH-84 and pPTH-87, with their difference only at 5 position 85 of the PTH gene. Plasmid pPTH-84 has the termination triplet codon at this position and plasmid pPTH-87 has cysteine codon.

Another expression plasmid pPTH-84c was constructed by digesting pPTH-84 with EcoRI and PstI to 10 remove the 5' portion of the PTH gene. The large restriction fragment bounded by EcoRI and PstI sites were isolated and ligated with six synthetic overlapping oligonucleotides which reconstructed the 5' end of the PTH gene with an ATG starting codon at amino acid-1. A 15 crossover linker sequence (Sung 1986b) was designed at the upstream end, which was homologous to the sequence encompassing the ribosomal binding site to the starting ATG of the β -galactosidase gene already present in the opposite terminus of the plasmid intermediate. After transformation 20 of E. coli JM103, the homologous termini recombined in vivo to yield plasmid pPTH-84c. The new plasmid pPTH-84c was present in 4% of all transformants. The construction of the plasmid in the region of the ribosomal binding site and PTH coding region was confirmed by nucleotide sequencing.

25

EXAMPLE 1: Synthesis of human PTH-coding nucleotide sequence with their PTH(1-5) domain rich in adenine, guanine, cytosine or thymine.

Using plasmid pPTH-84, we designed and 30 synthesized various PTH nucleotide coding sequences in two separate segments, namely PTH-(1-28) and PTH-(29-84). As nucleotide coding sequence for the segment PTH-(29-84), namely the mid to C-terminal region, we used the abovementioned sequence constructed with yeast-favored 35 codons, described by us previously in plasmid pPTH-84.

Using standard published protocols, the abovementioned precursor plasmid pPTH-84 previously

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described by us (see Preliminary Example), was linearized by endonucleases PstI and EcoRI (Maniatis 1982). The PstI/EcoRI-linearized plasmid containing the PTH-(29-84) sequence was utilized for the construction of new PTH genes
5 with different oligonucleotide contents at the amino terminus, as referred to below. The linearized plasmid was dephosphorylated with calf intestine alkaline phosphatase (CIAP) according to Maniatis. The PstI/EcoRI/CIAP-treated plasmid pPTH-84 was used directly for the construction of
10 novel plasmids.

Various coding sequences of the segment PTH-(1-28) were constructed. These were designed so as to demonstrate the effect of varying available degenerate codons while at the same time encoding the normal human PTH amino acid sequence at positions 1 through 28. In order to achieve this, a series of oligonucleotides encoding amino acids 1 through 8 of PTH were designed using the various degenerate codons available for the specified amino acids.
15 Each oligonucleotide was selected so as to have the maximum number of adenine (A) molecules in the first five codons, as well as, for comparative purposes, the maximum number of each of cytosine (C), guanine (G) or thymine (T) in the first 5 codons. Thus the N-terminal amino acid (1-5) sequence of PTH namely (methionine)-serine-valine-serine-
20 glutamic acid-isoleucine... could be encoded by the various synthesized nucleotide sequences illustrated in
25 Table 1.

In the result, we synthesized a series of oligonucleotides encoding PTH-(1-8), namely P1AA, P1CC,
30 P1GG, and P1TT, rich in each of the specific nucleotides A, C, G and T, at coding positions 1 through 5.

Complementary oligonucleotides encoding PTH-(1-8), namely P8AA, P8CC, P8GG and P8TT, were also synthesized with each possessing a homology-searching sequencing for subsequent integration with the
35 ribosome-binding sequence in the plasmid.

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An oligonucleotide duplex (P2B/P7B) was designed to encode PTH-(9-17). In this example, that oligonucleotide duplex was not designed with any effort to make it rich in a specific nucleotide. A further 5 oligonucleotide duplex (P3/P6) was similarly designed to encode PTH-(18-28). These synthetic oligonucleotides encoding PTH-(1-8), PTH-(9-17) and PTH-(18-28) together reconstruct the amino end (1-28) of the human PTH gene. A cross-over linker sequence COL-1 is designed at the amino 10 end which is homologous to the abovementioned complementary sequence encompassing the ribosome-binding site for the starting codon already present in the plasmid pPTH-84. The two homologous termini are capable of recombining in vivo to obtain plasmid pPTH-AA, and in similar fashion, pPTH-CC, 15 pPTH-GG, and pPTH-TT as described below.

This procedure is illustrated for pPTH-AA in Figures 3, 4 and 5. In Figure 3, the nucleotide sequence of the synthesized (1-5) adenine-rich oligonucleotide duplexes is set out. The construction of plasmid pPTH-AA therefrom is illustrated in Figures 4 and 5. With reference to Figures 3, 4 and 5, overlapping 20 oligonucleotide duplexes COL-1, P1AA, P2B, P3, P6, P7B, P8AA (hatched in Figure 4), constituting the coding sequence of PTH-(1-28), were ligated to the PstI end of the 25 linearized plasmid pPTH-84. The homology-searching sequence of the COL-1/P8AA duplex (black in Figure 4) recombines with the identical ribosome-binding site (black) of the gal gene at the opposite plasmid terminus in vivo during transformation of E. coli. The plasmid was 30 circularized to yield new plasmid pPTH-AA with the residual gal gene (stippled in Figure 4) deleted.

In summary, the constructed A-, C-, G- or T-rich oligonucleotides encoding amino acids 1 through 8 were, separately, phosphorylated together with the cross-over 35 linker COL-1, the oligonucleotide encoding amino acids 9 through 17, and the oligonucleotide encoding amino acids 18 through 28. The phosphorylation solution contained 0.23 mM

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ATP, 70 mM Tris-HCl pH 7.6, 10 mM MgCl₂, 100 mM KCl,
5 mM DTT and 30 U of T₄ DNA kinase at 37°C for 1.6 hr. The
complementary oligonucleotides were phosphorylated under
identical conditions. The two phosphorylation solutions
5 were combined and heated at 80°C for 12 minutes. The
combined solution was cooled slowly to 22°C in a water bath
to ensure annealing of the oligonucleotides. This mixture
was added to a 7 µl solution containing 75 mM Tris-HCl pH
10 7.5, 7.5 mM MgCl₂, 12.5 mM DTT, 1.2 mM ATP, 2 U of T₄ DNA
ligase and 50 ng (0.025 pmol) of the PstI/EcoRI/CIAP-
treated plasmid pPTH-84. After incubation at 12°C for 16
hours, this ligation mixture was used to transform E. coli
JM103 on YT plates (8g Bacto-Tryptone, 5g Bacto-Yeast
Extract, 5g NaCl, 15g Bacto-Agar all in 1 litre) containing
15 100 µg ampicillin/ml, following the protocol described by
Maniatis. Transformants were regrown on nylon filters
(Magna, MSI) on YT ampicillin plates for 16 hours. The
colonies were denatured with 0.5 M NaOH-1.5 M NaCl (10
mins.) and neutralized with 0.5 M Tris- HCl (pH 7.0) - 1.5
20 M NaCl (10 mins.). After 2 hrs. at 80°C in a vacuum oven,
the filters were washed for 30 mins. with SSC soln. which
was made of sodium chloride (52 g/L), sodium citrate (29
g/L) and 0.05% Triton X-100. Cell debris was removed
completely from the filter. The filter was placed into the
25 10 mL of SSC solution, which also contained 1% dextran
sulphate, Ficoll (100 mg/L), polyvinylpyrrolidone (100
mg/L) and bovine serum albumin (Fraction V, 100 mg/L).

For the construction of plasmid pPTH-AA, the ³²P-
labelled probe P8AA (10 pmol) was used to identify clones
30 containing the new plasmid pPTH-AA. After 16 hrs. at 45°C,
the filter was washed with SSC solution at 65°C for 30
mins., followed by autoradiographic analysis. Of 425
transformants tested, 61 retained affinity to the labelled
35 probe P8AA (mutant population 14%) and were selected for
preparation of plasmids. Nucleotide sequencing by the
well-established dideoxytermination method confirmed the
construction of plasmid pPTH-AA which possessed an A-rich

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N-terminal coding sequence properly integrated to the ribosome-binding site of, in this case, the lac promotor.

Other plasmids such as pPTH-TT, pPTH-CC, and pPTH-GG were also constructed with the same protocol. For 5 generating the maximum number of a specific nucleotide (C, G or T) in the PTH-(1-5) region, appropriate oligonucleotide duplexes encoding the PTH-(1-8) region were used instead of the P1AA/P8AA duplex.

Each transformant was cultured in 5 ml of a 2YT 10 medium (16 g Bacto-Tryptone, 10 g Bacto-Yeast Extract and 10 g NaCl in a litre) additionally containing ampicillin (100 mg/L) and isopropyl β -D-thiogalactoside (final concentration 0.7 mM) at 37°C for 10 hours. Cells were harvested after centrifugation. A 1% SDS solution (1.25 15 ml) was added. The cells were lysed by sonication. The PTH content was estimated by the 2-site Allegro PTH Radioimmunoassay following the manufacturer's instructions.

A comparison of the yields of the transformants 20 produced using each of the constructed plasmids revealed that the A-rich N-terminal sequence in plasmid pPTH-AA resulted in a dramatic increase in yield of immunoreactive PTH, for example when compared with the yield of plasmid pPTH-84c, as illustrated in Table 1. These comparisons 25 show that substantially higher yields of PTH are obtained using plasmids rich in adenine at nucleotide codons encoding amino acids 1 through 5, when compared with other PTH plasmids under the control of the same promoter.

Both plasmids pPTH-CC and pPTH-TT, with PTH-(1-5) 30 coding sequences rich in C and T, generate PTH with low efficiency consistent with those previously described by Breyel and Rabbani, despite the fact that in the case of pPTH-TT the five codons (TCT-GTT-TCT-GAA-ATA) encoding the PTH-(1-5) region are so-called E. coli-favoured codons 35 (Grantham 1980). The G-rich N-terminal sequence of plasmid pPTH-GG initially appeared to generate a higher yield of an immunoreactive PTH substance (estimated by Allegro RIA),

however, further studies revealed that the product included a large proportion of biologically inactive PTH fragments namely PTH-(8-84).

Since the first and third amino acid residues in
5 PTH are serine, six different degenerate codons are available for coding it. Plasmid pPTH-CompB was constructed in the same fashion as above described using the AG-containing codon for serine as opposed to the TC-containing codon used to construct plasmids pPTH-AA,
10 -CC, -GG and -TT (see Table 1). Using this codon, yield of intact PTH was generally improved (see Table 1), although lower than when using plasmid pPTH-AA.

15 EXAMPLE 2: Synthesis of human PTH-coding nucleotide sequences with PTH-(1-28) domain rich in adenine and plasmids containing them.

We next sought to establish whether there would be any effect of enhanced adenine richness at sites other than those coding for amino acids 1 through 5. Using the
20 same procedure as already described, and plasmid pPTH-84 synthesized using yeast-favoured codons, we constructed plasmids pPTH-wA and pPTH-wxA containing additional adenine richness at various codons between positions 12 and 28, as illustrated in Table 1. As set out in Table 1, the estimated PTH yield using pPTH-wA and pPTH-wxA was a
25 similar order to that obtained using pPTH-AA. It will be noted that in both cases, there was no improvement in yields of human PTH over that obtained by plasmid pPTH-AA. This suggests that only adenine immediately downstream from
30 the starting codon ATG exerts the noted positive effect on expression.

EXAMPLE 3: Effect of adenine richness at various of the (1-5) codons.

35 Using the same methods, we also constructed plasmid pPTH-hA, with its PTH-(1-5) codons identical to those of human PTH cDNA (i.e. (ATG)-TCT-GTG-

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AGT-GAA-ATA...). The nucleotide sequence for the N-terminal end of pPTH-hA is indicated in Table 1. Codons 3 to 5 but not 1 and 2 are adenine-rich. This plasmid resulted in a relatively low yield of PTH. This suggests 5 that adenine richness in codons 1 and 2 is important in obtaining the improved yield of intact PTH according to this invention.

EXAMPLE 4: Effect of E. coli-favoured degenerate codons 10 dominating in PTH-(29-84).

Plasmid pPTH-AA-Eco was also constructed using nucleotide sequence dominated by E. coli-favoured degenerate codons for encoding the mid through C-terminal regions PTH-(29-84) (Chen 1982). By the procedure 15 previously described, plasmid pPTH-AA was linearized using endonucleases PstI and HindIII. Oligonucleotides P103b, P104, P105, P106, P201, P202, P203 and P204a constituting a PTH-(29-84) coding sequence adapted predominantly from degenerate codons in the usage frequency favoured by E. 20 coli, as described in Figure 6 were ligated into the PstI/HindIII-treated plasmid as illustrated in Figure 7. The new plasmid, pPTH-AA-Eco was, when expressed in a transformed host, capable of somewhat higher yields (5.5 mg/L as shown in Table 5) in E. coli JM103 under the induction of isopropylthiogalactoside (IPTG) than plasmid 25 pPTH-AA which possessed yeast-favoured frequency of codon usage in PTH-(29-84) coding sequence.

We then carried out the same experiment by constructing two plasmids pPTH-AA-Eco(18-84) and 30 pPTH-AA-Eco(8-84) with the same codons (1-5) as pPTH-AA-Eco, but with E. coli-favoured codons encoding PTH-(18-84) and PTH-(8-84) regions respectively. The former obtained substantially the same yield of intact PTH in transformed E. coli strain JM103 as plasmid pPTH-AA-Eco, 35 while the latter had a substantially lower yield.

Table 2 summarizes the structure of various synthesized plasmids which possess identical PTH-(29-84)

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nucleotide sequence constituted by E. coli-favoured codons, as well as the intact PTH yield of E. coli Y1091 transformed with such plasmids.

We conclude that further extending the 5 E. coli-favored frequency of codon usage in the coding sequence upstream from amino acids 28 to 8 of PTH has little or no positive effect on the expression of intact PTH in E. coli. Indeed substitution of the adenine rich codons in regions of the N-terminal coding sequence with 10 codons favoured by E. coli can decrease the yield of PTH as, for example, in the case of plasmids pPTH-AA-Eco(8-84) and pPTH-TT whose T-rich codons 1 through 5 are generally those favoured by E. coli for the amino acids 1 through 5 encoded.

15 The same PTH-(29-84) nucleotide sequence of pPTH-hA-Eco, however, failed to improve the yield of PTH, thereby indicating an inefficiency of its N-terminal PTH-(1-5) coding sequence, which is identical to that of human cDNA.

20 **EXAMPLE 5:** Effect of internal starting codon and ribosome-binding sites on PTH expression

The analog PTH-(8-84), a byproduct of expression, can theoretically be derived via (i) proteolytic degradation of intact PTH, or (ii) internal initiation of expression at ATG-8. As in plasmids pPTH-GG, pPTH-GG-Eco, 25 pPTH-hA-Eco and pPTH-84c which produce such analog, their codons in the PTH-(2-5) region may have constituted a ribosome-binding site to initiate competing expression at the codon ATG-8. For the confirmation of such possibility, more new plasmids were constructed, with their degenerate 30 codons constituting various potential ribosome-binding sites at the PTH-(1-5) domain (Table 3). After expression, the ratio of intact PTH and the analog PTH-(8-84) was determined by Western immunoblot with antibodies specific 35 to the PTH-(69-84) region. As predicted, the production of fragment PTH-(8-84) is confined to plasmids which possess a

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potential ribosome-binding site (G-rich sequence interspersed by A, i.e. as described in Shine 1974) in the PTH-(2-5) region, without any exception.

Among plasmids which exclusively produce intact PTH, the most efficient plasmids were pPTH-AA-Eco and pPTH-CompE-Eco, both possessing the highest adenine composition in the N-terminal coding region. However, the expression efficiency was decreased when adenine of the degenerate codons was substituted by other bases, especially with cytosine and thymine (Table 3).

Among the remaining plasmids which produce both intact PTH and PTH-(8-84), the proportion of intact PTH in the mixture also decreased with the substitution of adenine in the PTH-(1-5) domain by other bases (Table 3). The most severe cases were in plasmids pPTH-GA11-Eco and pPTH-GA12-Eco where adenine of codons 1 and 2 was substituted by cytosine and thymine. Though encoding intact PTH, plasmid pPTH-GA12-Eco produces exclusively fragment PTH-(8-84), without any trace of intact PTH detected. Apparently this is a result of two factors, (i) poor expression of intact PTH because of low adenine composition in the N-terminal region, and (ii) a strong internal ribosome-binding site favoring the expression of PTH-(8-84). Therefore, our data confirm that the nucleotide sequence encoding the PTH-(1-5) region predetermines both the potential expression of the short analog and the expression efficiency for intact PTH.

While synthetic PTH genes were used in our laboratory, all prior studies of PTH expression in E. coli by other researchers, involved the human PTH cDNA. However, the human PTH cDNA possesses a ribosome-binding site-like sequence GTG.AGT (underlined) in the PTH-(2-3) region, for the potential expression of PTH-(8-84). In the expression of the human preproPTH cDNA in E. coli, the short analog PTH-(8-84) was indeed obtained as a byproduct (Born 1987b). In another earlier study, a PTH-(1-84) nucleotide sequence (without the prepro sequence) derived

from cDNA has been used for expression in E. coli, by other laboratories (Breyel 1984). Although an immunoreactive PTH product was produced at 0.2 mg/L (estimated by PTH radioimmunoassay) under the control of a lac promotor, its identity has never been properly established. It is highly probable that the uncharacterized product of this earlier study was a mixture of intact PTH and PTH-(8-84). Such a possibility of competing expressions of intact PTH and PTH-(8-84) were further supported by the expression of our plasmids pPTH-hA-Eco and pPTH-hA. Both were constructed with the codons at the PTH-(1-5) domain identical to those of human PTH cDNA (Breyel 1984). As predicted, under the control of a lac promotor, expression yielded a 2:1 mixture of intact PTH and the analog PTH-(8-84) with a total yield of 0.2-0.3 mg/L (Tables 1, 2 and 3, Figure 10). All these results thus indicate that the cDNA-derived PTH coding sequence is undesirable for direct expression in E. coli, because of its poor expression efficiency and the competing production of PTH-(8-84). In addition, such byproduct would complicate any subsequent purification of intact PTH.

EXAMPLE 6: Selection of appropriate host cell and expression conditions.

In testing the expression of our constructed plasmids, we transformed various E. coli strains with them as illustrated in Tables 4 and 5. E. coli strain Y1091, when transformed with our plasmids, generally expressed PTH at a yield considerably greater than that of similarly transformed JM103 and HB101, in terms of mg PTH/L culture and percentage of total bacterial protein. Increased culture periods beyond 10 hours at 37°C, were, in general, not found to be an effective means of improving yields (see Tables 5 and 6). Once the optimum culture period had expired, longer culture periods generally only proved detrimental to yield. Our study of bacterial hosts used for expression of our synthesized plasmid clearly indicates

that E. coli Y1091 was consistently superior to other commonly used E. coli strains. Such improvement in PTH production by host substitution (to lon strain) contradicts the results of Breyel.

5 In JM103 transformants, the induction of the lac promoter was essential for PTH expression. However, induction was not needed in the lon strain Y1091. The PTH gene, though under the control of the lac promoter, does not require induction of isopropylthiogalactoside (IPTG) in 10 Y1091 (see Table 5). The exclusion from the culture medium of isopropylthiogalactoside which is an expensive reagent would be economically beneficial to any large scale 15 production of PTH, thus E. coli Y1091 is to be preferred for that reason as well as for its improved yield and ratio of intact PTH to total bacterial protein.

Our studies related to the establishment of culture conditions for optimal expression of PTH are summarized in Table 6. We carried out a time study of the production of PTH by E. coli Y1091 transformed by plasmid 20 pPTH-AA-Eco. The expression was carried out at 37°C, in 2YT medium in the presence of 1% Casamino acids. Maximum yield was obtained after permitting expression intracellularly for 10 hours.

25 EXAMPLE 7: Analysis of expressed PTH by gel electrophoresis.

The products expressed by different E. coli Y1091 transformants were analyzed. Transformants possessing plasmids pPTH-AA-Eco and pPTH-GG-Eco and were 30 cultured in 2YT + 1% Casamino acids, 100 mg ampicillin/L, at 37° for 10 hours. Cells harvested after centrifugation were lysed by 1% SDS. Electrophoresis of total cell lysate was carried, out on 1% SDS - 17% polyacrylamide gel (14x16 cm, 1mm) (stained by Coomassie blue). Application dosage 35 of each sample was equivalent to 40 µl of the original culture. The results are illustrated in Figure 8, where

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numbers in left margin indicate molecular weight standards.

- 5 Lane a - clone with plasmid pUC8 with no PTH gene
 (negative control)
- 10 Lane b - clone with plasmid pPTH-GG-Eco producing
 PTH-(8-84).
- 15 Lane c - clone with plasmid pPTH-AA-Eco producing
 intact PTH.
- 20 Lane d - clone with plasmid pUC8 plus synthetic
 intact PTH.
- 25 Lane e - synthetic intact PTH.
- 30 Lane f - purified recombinant PTH.

15 EXAMPLE 8: Immunological (Western) blot characterization
 of PTH expressed by E. coli.

20 Antibodies specific to amino and carboxyl termini
 of PTH were prepared as follows. PTH-(69-84) amide was
 synthesized on methybenzhydrylamine resin, using tBoc
 chemistry (Stewart 1984). PTH-(1-17) was constructed on a
 branched lysine core as described (Posnett 1988). The core
 was constructed on a phenylacetamidomethyl resin, with a
 β -alanyl spacer, and using bis-tBoc-Lys. Rabbit antibodies
 were developed directly to the PTH-(1-17)-Lys complex and
 to PTH-(69-84) coupled to keyhole Limpet hemocyanin. The
 antibodies were affinity purified by passage through a
 column of PTH-(1-17) coupled to AffiGel 15 or PTH-(69-84)
 coupled to AffiGel 10.

25 The protein products of different transformants
 were analysed by an immunoblotting procedure. Whole cell
 lysates of E. coli Y1091: pPTH-AA-Eco and Y1091:pUC8 were
 committed to electrophoresis on 1% SDS - 17% polyacrylamide
 gel (14x16 cm, 1mm) as described in detail in Example 8
 (except using 24 μ l of culture). Without staining, the
 protein contents were electro-transferred from the gel onto
 two nitrocellulose membranes which sandwiched the gel (200
 mamp, 15 min. and then current reversed for 45 min.). The

membranes (Towbin 1979) were saturated with 10% fetal calf serum, and were immunoblotted separately with the anti-PTH-(69-84) antibodies (Figure 9A) and the anti-PTH-(1-17) antibodies (Figure 9B). After standard treatment in substrate solution (nitro blue tetrazolium and 5-bromo-4-chloro-3-indolyl phosphate, 30°, 20 min.), dark bands could be observed, indicating PTH-related protein. The results are indicated in Figure 9, where the numbers in the left margin show molecular weight standards, as well as the positions of intact PTH and analog PTH-(8-84).

Lane a - E. coli Y1091:pUC8 (negative control)
Lane b - E. coli JM103:pPTH-GG.
Lane c - E. coli Y1091:pPTH-GG-Eco
Lane d - E. coli JM103:pPTH-AA
Lane e - E. coli Y1091:pPTH-AA-Eco.
Lane f - E. coli purified recombinant PTH
Lane g - synthetic intact PTH from Bachem Ltd.

EXAMPLE 9: Characterization of intact PTH expressed by E. coli strain Y1091, transformed by plasmid pPTH-AA-Eco.

(a) Radioimmunoassays were carried out according to known procedures. Both estimations by the Mid-molecule PTH Radioimmunoassay and the Allegro PTH Radioimmunoassay were identical, indicating all recombinant PTH was likely in the form of intact molecule.

(b) Gel electrophoresis of a lysate of clone Y1091: pPTH-AA-Eco on SDS-polyacrylamide gel (stained by Coomassie blue dye) indicated only a single new band. It has the same mobility as synthetic human PTH (manufactured by Bachem Ltd.). (See Figure 8).

(c) Western blotting with antibody specific to PTH-(1-17) as in Figure 9B or PTH-(69-84) as in Figure 9A confirmed the new polypeptide as PTH-(1-84). Short analogs, such as PTH-(8-84) previously reported (Born 1987b; Rabbani 1988), were not detected.

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(d) The yield of intact PTH in this system (20 mg/L or 2.5% of total bacterial protein) is 50-100 fold better than results of Breyel and Rabbani.

Exclusive production of PTH-(1-84) was also confirmed in transformants possessing plasmids pPTH-AA, 5 pPTH-CompB, pPTH-wA-Eco, pPTH-A-Eco(18-84), pPTH-A-Eco(8-84), and pPTH-CompE-Eco.

Our PTH gene of plasmid pPTH-AA-Eco lacks the structural features common in some highly expressed genes 10 (Gold 1981). Sometimes the efficiency of translation of some genes can be improved by the elimination (or weakening) of secondary structure in the mRNA (Hall 1982; Tessier 1984). In the PTH mRNA of plasmids pPTH-CC and pPTH-TT, hairpin loops can potentially be formed between 15 the A,G-rich ribosome-binding site and the amino-terminal region with respective ΔG (free energy) values of -7.0 and -9.6 kcal (Tinoco 1973), to interrupt the translation process. The A-rich degenerate codons in the PTH-(1-5) region of plasmid pPTH-AA, may weaken such secondary 20 structure ($\Delta G = -3.2$ kcal) and consequently improve PTH expression. However, such mechanism fails to explain the poor PTH expression by plasmid pPTH-84c, which has a similarly weakened secondary structure in its PTH mRNA ($\Delta G = -3.4$ kcal).

In addition, five codons TCA-1, GTA-2, TCA-3, 25 ATA-5 and TTA-7 at the PTH N-terminus of plasmids pPTH-AA and pPTH-AA-Eco (Tables 1 and 2), are considered to be rare degenerate codons in E. coli (Chen 1982). The more efficient PTH production by these two plasmids, as compared 30 to others, contradicts earlier conclusions that tandem repeats of minor degenerate codons (Varenne 1986) and their proximity to the initiation codon would dramatically reduce the maximal level of protein synthesis (Chen 1990).

Comparison of the plasmids pPTH-AA, pPTH-CompB, 35 pPTH-AA-Eco, pPTH-CompE-Eco, pPTH-GG and pPTH-GG-Eco with the other plasmids less efficient in PTH expression (Tables 1 and 2), indicates that the efficiency of expression might

be determined by the nucleotide (adenine, and likely to a small extent, guanine) composition of the amino-terminal coding sequence.

- 5 EXAMPLE 10: Characterization of PTH-(8-84) expressed by E. coli strain Y1091, transformed by pPTH-GG-Eco and other plasmids.

A series of new PTH genes were constructed with different previously constructed N-terminal (1-28) coding 10 sequence truncated to the PTH-(29-84) coding sequence dominated by degenerate codons in the usage frequency favoured by E. coli. This was easily accomplished by ligating the PstI/HindIII-cut PTH-(29-84) coding sequence of pPTH-AA-Eco, which was isolated after PstI and HindIII 15 restriction, to any of the PstI/HindIII-linearized plasmids described earlier (e.g. pPTH-wA, pPTH-GG and pPTH-hA, etc.). This would demonstrate the combined effect of E. coli-favoured codons in the mid/carboxyl section and host substitution.

20 E. coli strain Y1091 clone transformed by plasmid pPTH-GG-Eco, with G-rich codons at the sites coding for amino acids 1 through 4 yielded predominantly the short fragment PTH-(8-84), with the yield of immunoreactive PTH increased to 25 mg/L or 3% of bacterial protein. These 25 results demonstrate that potential ribosome binding sites upstream from codon ATG at position 8 enhance its misreading as a start codon.

Gel electrophoresis of a lysate of clone Y1091:pPTH-GG-Eco indicated mainly a new polypeptide more mobile than the synthetic human PTH (Figure 8), and it was eventually identified as PTH-(8-84) (Born 1987b). Western blotting with anti-PTH-(69-84) antibodies revealed the immunoreactive product as predominantly the short analog, mixed with some PTH-(1-84) (Figure 9A). Blotting with the 35 anti-PTH-(1-17) antibodies showed a dramatic loss of immunoreactivity of PTH-(8-84) in this lysate (Figure 9B), due to the loss of amino acid residue (1-7). The same

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immunoreactive mixture was also observed in transformant possessing plasmid pPTH-GG (Figure 9). These results have indicated that even the Allegro PTH RIA does not exclude PTH-(8-84) in the estimation of PTH.

5 Western blot of cell lysate from clones Y1091:pPTH-hA-Eco and JM103:pPTH-hA also showed a 2:1 mixture of intact PTH and PTH-(8-84). Figure 10 illustrates Western immunoblotting of PTH product expressed by plasmids pPTH-hA and pPTH-hA-Eco. The membrane was 10 immunoblotted with antibody specific to PTH-(69-84). All samples were whole cell lysates. Molecular weight standards are on the left margin.

Lane a - Y1091:pPTH-GG-Eco, 1 μ l culture.

15 Lane b - mixed lysates of Y1091:pPTH-GG-Eco and Y1091:pUC8, 1 and 60 μ l respectively.

Lane c - Y1091:pPTH-hA-Eco, 56 μ l.

Lane d - JM103:pPTH-hA, 50 μ l.

Lane e - Y1091:pUC8, 60 μ l.

Both plasmids pPTH-hA and pPTH-hA-Eco yielded a 2:1 mixture 20 of intact PTH and PTH-(8-84) (Lanes c and d).

In another clone pPTH-GA3-Eco which had only one G-rich codon TCG for amino acid one and A-rich codons for amino acids 2 through 4, moderate yield (8 mg/L) of intact PTH was detected without formation of PTH-(8-84), thereby 25 further establishing the essential role of an A-rich degenerate codon at the first amino acid for the efficient expression of intact PTH and the absence of an efficient ribosome-binding site in amino acids 2 to 4 in avoiding expression of PTH-(8-84) fragment.

Since GTG, CTG and TTG have been used as a minor starting codon in some genes, any TG dinucleotide sequence in the PTH-(1-7) region may constitute a starting triplet codon in any reading frame resulting in competing translation, and reduction of expression of PTH. The 35 absence of any such potential start codon in the PTH-(1-7) region in clones pPTH-AA, pPTH-AA-Eco, and pPTH-GA3-Eco,

etc., may partially account for the successful expression of intact PTH by E. coli transformed with these plasmids.

EXAMPLE 11: Synthesis of PTH analog.

We also carried out tests designed to produce PTH having greater stability and longer half-life. Typically, intact human PTH contains glycine as the amino acid residue at position 38. We have designed and produced a "mutant" PTH which, instead, contains an aspartic acid at position 38. Since the biological activity of PTH is believed to be located in the region of amino acids 1 through 34, accordingly a modification of the amino acid at position 38 should not alter the biological activity of our synthesized PTH. It should, however, increase the stability of the polypeptide during production in E. coli and its half-life in clinical application because aspartic acid at position 38 strengthens the potentially weak glycine-38 linkage. We constructed a plasmid PTH-AA-Eco-ASP-38 with codon GAC for aspartic acid-38, substituting GGC for glycine-38 in pPTH-AA-Eco to express this mutant form of PTH. Expression of the mutant plasmid in E. coli Y1091 was consistently higher than that of pPTH-AA-Eco (30 milligrams per litre compared with 20 milligrams per litre). Moreover it demonstrated its survivability or stability during PTH production in E. coli. The asp-38 mutant protein has the same mobility as synthetic intact PTH (from Bachem Ltd.) on SDS-polyacrylamide gel electrophoresis with Coomassie blue stain. The N-terminus was sequenced and confirmed identical to human PTH up to 40 amino acid residues, with the exception of an aspartic acid residue at position-38. The amino acid composition analysis (by %) was identical to the theoretical calculation.

Example 12: Extraction and purification of recombinant PTH.

After harvesting from culture medium by centrifugation, cells were sonicated (1 min, pulsed) at 4°C

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in a mixture (1 ml/g) of 1 M HCl containing 1% (w/v) NaCl, and 1% (v/v) TFA (Rabbani 1988) and centrifuged. The cell debris was reextracted a second time in the same fashion. The two extracts were pooled. This acidic extraction of 5 E. coli Y1091:pPTH-AA-Eco enriched PTH-(1-84) to 10% of the total protein (60% recovery) (Rabbani 1988). The extract was adjusted to pH 3.8 with sodium hydroxide, diluted with water (4:1), and applied to a HL 10/10 Mono S column 10 (Pharmacia) (Figure 11A is a chromatogram of the extract on cation exchanger Mono S, with concentration of PTH (black dots) in collected 1 ml. fractions estimated.) The column was eluted with a gradient of 0-2 M NaCl in 50 mM formic acid (pH 3.8) and PTH was recovered at 55% as evaluated by RIA. Immunoreactive fractions were pooled and applied to a 15 1x25 cm C₁₈ silica (10μm) column (Vydac) (Rabbani 1988). It was then eluted with a 1% /min gradient of 0.1% TFA/acetonitrile in 0.1% TFA/water (Figure 11B is a chromatogram of subsequent HPLC purification on C₁₈ silica, with PTH-containing peak (stipple) indicated.

20 Immunoreactive fractions containing mainly intact PTH were combined and lyophilized to yield intact PTH as a homogeneous product. The HPLC on C₁₈ silica, which was capable of separating intact PTH, the unprocessed fMet-PTH, and analog PTH-(8-84) in a gradient of acetonitrile in 0.1% 25 TFA (Rabbani 1988), revealed intact PTH as the only PTH-moiety isolated. Its purity was also confirmed by both gel electrophoresis (Figure 8) and Western blots (Figure 9). From 2 liters of culture medium, 6 mg of the recombinant intact PTH was obtained after lyophilization, 30 with an overall recovery of 15%.

EXAMPLE 13: Characterization of purified intact PTH.

(a) Amino Acid Composition Analysis - Amino acid composition analyses of protein and of purified peptides 35 were performed with a Durum D-500 Analyzer. Samples (100 μg) were hydrolyzed in vacuo at 110°C in 6 N HCl for 24, 48 and 72 h and the data extrapolated to 0 h to correct

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for hydrolytic losses. Tryptophan was determined following hydrolysis in 4 N methane sulphonic acid containing 0.2% 3-(2-aminoethyl)indole at 110°C for 20 h in vacuo (Simpson 1976). The combined cystine and cysteine content was 5 determined after oxidation to cysteic acid (Hirs 1967) a hydrolysis in 6 N HCl at 110°C for 24 h.

Amino acid composition of the purified intact PTH was identical to the expected value for human PTH-(1-84) as summarized in Table 7 (Hendy 1981). In repeated analyses, 10 values of 1.95, 1.91, 2.07 and 2.09 were obtained for the number of methionine residues after hydrolysis of 24 h (Table 7), thus generally consistent to the predicted value of 2 for the processed intact PTH (Hendy 1981). Methionine sulfoxide, which has been detected in some recombinant 15 polypeptides secreted by E. coli (Hartmanis 1989), was not observed in the hydrolysed residues of PTH. Our data thus ruled out the presence of any significant amount of the oxidized Met-8, Met-18, or the unprocessed fMet.

For the production of the fully processed intact 20 PTH, Ser-1, the residue adjacent to fMet, has a small radius of gyration essential for the efficient removal of fMet residue from the nascent polypeptide (Sherman 1985; Levitt 1976).

(b) Amino Acid Sequencing - PTH samples (500 pmole) on 25 polyvinylidene difluoride membrane were analysed via gas-phase sequencing (Matsudaira 1987). Sequencing analysis of the purified intact PTH confirmed that the 40 residues at its amino-terminus was identical to that of human PTH-(1-84) (Hendy 1981). For sequencing other regions, the 30 recombinant intact PTH was initially digested with endoproteinase Asp-N (Boehringer Mannheim), which has been reported to cleave specifically at the amino-terminus of the aspartic acid residues. The resulting peptide mixture was separated by HPLC on C₁₈ silica using a 1% /min 35 gradient of acetonitrile in 0.1% TFA/water. After sequencing, one short peptide revealed a sequence of 11 amino acid residues identical to the PTH-(74-84) terminus

(Hendy 1981). The amino acid sequences of other analogs PTH-(8-84) and PTH-(3-84) were also established by the same analytical method.

(c) HyperMass Molecular Weight Determinations -

5 IonSpray mass spectra of the purified recombinant PTH-(1-84) and the PTH-(8-84) analog were obtained by the API III System (SCIEX, Mississauga, ONT). Ionspray mass spectra of recombinant PTH-(1-84) (Figure 12A) and analog PTH-(8-84) (Figure 12B) predominantly showed peaks of the 10 molecular ions possessing different numbers of positive charge (H^+). Based on the m/z value (i.e. mass/charge) and the charge number (z, indicated in parenthesis) of individual peaks, the molecular mass was calculated by the formula of $(m/z \times z) - z$ in four most prominent peaks. In 15 the spectrum of PTH-(1-84) (Figure 12A), molecular mass of 9424.90, 9425.91, 9426.91 and 9424.92 Daltons was obtained, with an average of 9425.66. In the spectrum of PTH-(8-84) (Figure 12B), molecular mass of 8668.30, 8668.71, 8669.01 and 8666.92 Daltons was calculated, with an average of 20 8668.73. The experimental molecular masses of 9425.66 Daltons for PTH-(1-84) and 8668.73 Daltons for PTH-(8-84), were thus consistent to their respective theoretical values of 9425.26 and 8668.36 Daltons. The absence of other unidentified ions in the mass spectrum (Figure 12A) of PTH-(1-84) generally confirmed the purity of this sample.

25 (d) Bioassay - With the identity and purity established, recombinant intact PTH (open circles) was compared with synthetic intact PTH (solid squares) (manufactured by Bachem Corp., Torrance, California) in an adenylate cyclase bioassay (Figure 13) (Rabbani 1988). This test involved the stimulation of adenylate cyclase by the PTH samples at different concentrations, to produce cyclic AMP in osteosarcoma cells (UMR 106). Cyclic AMP is a secondary messenger in the functional pathway of this 30 hormone. Our experimental results indicated average k_{act} values (PTH concentration for achieving half maximal stimulation) of 1.6 nM (k_{act} range 1.5- 1.7

nM) for our recombinant intact PTH, and 3.8 nM (range 3.5-4.2 nM) for the synthetic intact PTH (Figure 13). In comparison, PTH-(1-84) samples previously prepared by various recombinant DNA methods (Breyel 1984; Hogset 1990; 5 Rabbani 1988; Wingender 1989), have been reported to have k_{act} values equal to the synthetic PTH-(1-84) standard. The small k_{act} (1.6 nM) of our recombinant PTH-(1-84), which was half the k_{act} (3.8 nM) of the synthetic standard, indicated our recombinant sample being 10 the most bioactive of any PTH-(1-84) sample reported to date, synthetic or recombinant DNA-derived. Its strong bioactivity also indirectly confirmed its integrity. Analogs, such as the nascent fMet-PTH and the methionine-oxidized intact PTH, if present in significant amount, 15 would have reduced the bioactivity of the recombinant PTH since both analogs have very weak bioactivity (Rabbani 1988; Tashjian 1964).

EXAMPLE 14: Adenine-rich Nucleotide Sequence at the N-terminal Region Enhanced Expression of Analog PTH-(3-84)

The strategy of using an adenine-rich nucleotide sequence in the N-terminal domain to enhance gene expression was also demonstrated in the case of PTH-(3-84) since it and other fragments of PTH may demonstrate 25 biological activity. The short analog PTH-(3-84) has previously been produced as a minor byproduct during the expression of the preproPTH cDNA in E. coli. For improving production of this analog, a plasmid pPTH-(3-84)-AA-Eco was designed to possess nucleotide sequence identical to that 30 of pPTH-AA-Eco, with the loss of the two codons TCA.GTA for residues Ser-1 and Val-2 of PTH. The new plasmid pPTH-(3-84)-AA-Eco was assembled in the same manner as the latter plasmid. Expression in strain Y1091 yielded PTH-(3-84) as the only PTH product at 15 mg/L. This was 35 confirmed by gel electrophoresis, Western immunoblotting and amino acid sequencing.

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Table 1

Expression of PTH genes possessing different amino-terminal nucleotide sequences in E. coli strain JM103.

PTH gene -containing plasmids	PTH ^a mg/L	N-terminal coding sequences ^b				
		1	2	3	4	5
		Ser	Val	Ser	Glu	Ile
pPTH-AA	3.9	TCA	GTA	TCA	GAA	ATA
pPTH-CC	0.15	C	C	C		C
pPTH-GG	10 ^c	G	G.	G	G	
pPTH-TT	0.25	T	T	T		T
pPTH-CompB	1.1	AGT	T	AGT		T
pPTH-wA ^d	3.4					
pPTH-wxA ^e	3.5					
pPTH-hA	0.3 ^f	T	G	AGT		
pPTH-84c ^g	0.19 ^f	G	T	T	G	C

^a Estimated by Allegro RIA.

^b Nucleotide sequence encoding the PTH-(1-5) region of pPTH-AA is presented. For other plasmids, only nucleotides different from pPTH-AA are presented in this Table. Codon differences in other regions are stated individually.

^c A 1:5 mixture of PTH-(1-84) and PTH-(8-84).

^d GTA-21 and TTA-24.

^e AAA-13, -26, -27, TTA-15, -24, TCA-17 and GTA-21.

^f A 2:1 mixture of PTH-(1-84) and PTH-(8-84).

^g GTG-8, AAC-10 and TTG-11; see Preliminary Example.

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Table 2

Expression of PTH genes possessing different amino-terminal nucleotide sequences in E. coli strain Y1091.

PTH gene -containing plasmids	PTH ^a mg/L (% protein)	N-terminal coding sequences ^b				
		1 Ser	2 Val	3 Ser	4 Glu	5 Ile
pPTH-AA-Eco	20 (2.5)	T	C	A	T	A
pPTH-wA-Eco ^c	15 (2)					
pPTH-A-Eco(18-84) ^d	14					
pPTH-A-Eco(8-84) ^e	7					
pPTH-CompE-Eco	12	A	G	C	A	G
pPTH-GG-Eco	25 ^f	G	G	G	G	
pPTH-hA-Eco	0.3 ^g	T	G	A	G	T

^a Estimated by Allegro RIA. Values in parenthesis () are yields as percentage of bacterial protein, calculated by integrating the areas under the peak after densitometric scanning of gel.

^b Nucleotide sequence encoding the PTH-(1-5) region of pPTH-AA-Eco is presented. For other plasmids, only nucleotides different from pPTH-AA-Eco are presented in this Table. Codon differences in other regions are stated individually.

^c GTA-21 and TTA-24.

^d CGT-20, -25, CTG-24 and AAA-27.

^e AAC-10, CTG-11, -15, -24, AAA-13, -26, -27, CGT-20, GTG-21 and CGC-25.

^f A 1:5 mixture of PTH-(1-84) and PTH-(8-84).

^g A 2:1 mixture of PTH-(1-84) and PTH-(8-84).

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Table 3

Effect of potential ribosome-binding site (underlined) in N-terminal coding region of different plasmids on the expression of intact PTH and PTH-(8-84) in E. coli Y1091.

Clone	PTH yield mg/L	N-terminal coding sequence							
		1	2	3	4	5	6	7	8
	intact	(8-84) ser val ser glu ile gln leu met							
pPTH-AA-Eco	20	TCA	GTA	TCA	GAA	ATA	CAA	TTA	ATG
pPTH-CompE-Eco	12	AGC	GTA	AGC	GAA	ATA			
pPTH-GA3-Eco	8.1	TCG	GTA	TCA	GAA	ATA			
pPTH-GA10-Eco	5.9	TCA	GTG	TCA	GAA	ATA			
pPTH-GA1-Eco	5.5	TCG	GTG	TCA	GAA	ATA			
pPTH-CC-Eco	0.3	TCC	GTC	TCC	GAA	ATC			
pPTH-TT-Eco	0.2	TCT	GTT	TCT	GAA	ATT			
pPTH-GA8-Eco	4.5	1.5	TCA	GTA	TCA	<u>GAG</u>	ATA		
pPTH-GA9-Eco	4.0	1.2	TCA	GTG	TCA	<u>GAG</u>	ATA		
pPTH-GA4-Eco	3.5	1.5	TCG	GTG	TCA	<u>GAG</u>	ATA		
pPTH-GA5-Eco	2.5	1	TCG	GTG	TCG	<u>GAA</u>	ATA		
pPTH-hA-Eco	0.2	0.1	TCT	GTG	<u>AGT</u>	GAA	ATA		
pPTH-GA6-Eco	4	20	TCA	GTA	TCG	<u>GAG</u>	ATA		
pPTH-GG-Eco	4	21	TCG	GTG	TCG	<u>GAG</u>	ATA		
pPTH-GA11-Eco	1	23	TCT	GTC	TCG	<u>GAG</u>	ATA		
pPTH-GA12-Eco		15	TCT	GTT	TCG	<u>GAG</u>	ATA		

— weak ribosome-binding site.

— strong ribosome-binding site.

Table 4

Expression of plasmids pPTH-AA, pPTH-wA and pPTH-wxA in E. coli strains JM103 and Y1091.

Plasmids	<u>JM103</u>		<u>Y1091</u>	
	Intact PTH* (mg/L)	% bacterial protein	Intact PTH* (mg/L)	% bacterial protein
pPTH-AA	3.9	0.5	6.5	0.8
pPTH-wA	3.4	0.4	7.0	0.9
pPTH-wxA	3.5	0.4	6.5	0.8

*Estimated by the Allegro PTH Radioimmunoassay

Table 5
Expression of PTH gene (plasmid PPTH-AA-Eco)
in different E. coli strains JM103, HB101 and Y1091.

Culture Conditions	JM103			HB101			Y1091		
	Intact PTH* (mg/L)	% bacterial protein	Intact PTH* (mg/L)						
8 hr [-IPTG]	0	0	7.1	0.9	20.0	2.5			
8 hr [+IPTG]	5.5	0.7	6.1	0.8	19.0	2.3			
16 hr [-IPTG]	0	0	1.7	0.02	0	0			
16 hr [+IPTG]	4.6	0.6	3.9	0.4	3.3	0.04			

*Estimated by the Allegro PTH Radioimmunoassay

Table 6

Production of PTH in E. coli Y1091: pPTH-AA-Eco,
in relationship to culture time.

Culture Time (hr.)	Intact PTH* (mg/L)	% bacterial protein
5	5.5	0.7
6	10.5	1.3
8	17.1	2.1
10	20.0	2.5
18	3.0	0.4

*Estimated by the Allegro PTH Radioimmunoassay.
Cells grown in 2YT medium without induction by IPTG.

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Table 7
Amino acid composition of the purified
recombinant intact PTH.

Amino acid	Residues/mol determined			nearest integer	pTH-(1-84)
	24h	48h	72h		
Asx	10.00	10.00	10.00	10 ^a	10
Thr	0.82	0.82	0.80	1	1
Ser	6.08	5.46	4.90	7 ^b	7
Glx	11.20	11.20	11.23	11	11
Pro	3.00	2.89	2.87	3	3
Gly	3.94	3.98	3.90	4	4
Ala	7.00	6.99	7.03	7	7
Cys	0.00			0	0
Val	7.97	8.04	7.86	8	8
Met	1.95 ^c	1.86	1.80	2	2
Ile	0.98	0.98	0.95	1	1
Leu	9.77	9.75	9.62	10	10
Tyr	0.00	0.00	0.00	0	0
Phe	0.99	1.04	1.03	1	1
His	4.04	4.09	4.06	4	4
Lys	9.07	9.04	9.01	9	9
Arg	4.95	5.03	4.97	5	5
Trp	1.06			1	1
Total				84	84

^a 10 Asx residues/mol is assumed.^b Extrapolated value of 6.7 at zero time.^c Values of 1.91, 2.07 and 2.09 obtained in repeated analyses.

CLAIMS:

1. A synthetic nucleotide sequence encoding intact human parathyroid hormone or a biologically active analog wherein at least some codons in the N-terminal region are selected from adenine-rich degenerate codons.
2. The nucleotide sequence according to claim 1 wherein codons encoding amino acids 1 through 28 are selected from adenine-rich degenerate codons available for coding such amino acids.
3. The nucleotide sequence according to claim 1 wherein codons encoding amino acids 1 through 5 are selected from adenine-rich degenerate codons available for coding such amino acids.
4. The nucleotide sequence according to claim 1 wherein codons encoding amino acids 1 through 3 are selected from adenine-rich degenerate codons available for coding such amino acids.
5. The nucleotide sequence according to claim 1 wherein codons encoding amino acids 3 through 5 are selected from adenine-rich degenerate codons available for coding such amino acids.
6. The nucleotide sequence according to claim 1 wherein codons encoding amino acids 2 and 3 are selected from adenine-rich degenerate codons available for coding such amino acids.
7. The nucleotide sequence according to claim 1 wherein the degenerate codons encoding amino acids 1 through 5 are TCA, GTA, TCA, GAA and ATA respectively.

- 44 -

8. The nucleotide sequence according to claim 1 wherein the degenerate codons encoding amino acids 1 through 3 are TCA, GTA and TCA respectively.

5 9. The nucleotide sequence according to claim 1 wherein the degenerate codons encoding amino acids 1 through 3 are TCG, GTA, and TCA respectively.

10 10. The nucleotide sequence according to claim 1 wherein the degenerate codons encoding amino acids 1 through 7 are selected so as to avoid coding for a potential ribosome-binding site.

15 11. The nucleotide sequence according to claim 1 wherein at least some of the codons encoding amino acids 29 through 84 are degenerate codons in the usage frequency favoured by Escherichia coli.

20 12. The nucleotide sequence according to claim 1 wherein at least some of the codons encoding amino acids 29 through 84 are degenerate codons in the usage frequency favoured by yeast.

25 13. The nucleotide sequence according to claim 1 wherein the codon encoding the amino acid 38 is selected so as to encode aspartic acid.

14. A plasmid containing the synthetic nucleotide sequence according to any one of claims 1 to 13.

30 15. An expression system comprising a microorganism transformed by the plasmid according to claim 14.

35 16. An expression system according to claim 15 wherein the microorganism is E. coli.

- 45 -

17. An expression system according to claim 15 where-in the microorganism is E. coli Y1091 (lon).

18. A method of obtaining intact human parathyroid hormone or a biologically active analog comprising transforming a microorganism with the plasmid of claim 14, and expressing and recovering intact human parathyroid hormone or a biologically active analog.

1/14

lac po

.....GAT AAC AAT TTC ACA CAG GAA ACA
CTA TTG TTA AAG TGT GTC CTT TGT

RBS

← Gal →

1 2
Ser Val

GCT ATG ACC ATG ATT ACG AA TTC TGT AAG GGA TCC AAG AAG AGA TCG GTT
 CGA TAC TGG TAC TAA TGC TT AAG ACA TTC CCT AGG TTC TCT AGC CAA

Eco RI

Bam HI

3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
Ser	Glu	Ile	Gln	Leu	Met	His	Asn	Leu	Gly	Lys	His	Leu	Asn	Ser	Met	Glu
TCT	GAG	ATC	CAA	TTG	ATG	CAT	AAC	TTG	GGT	AAG	CAC	TTG	AAC	TCT	ATG	GAA
AGA	CTC	TAG	GTT	AAC	TAC	GTA	TTG	AAC	CCA	TTC	GTG	AAC	TTG	AGA	TAC	CTT

20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36
Arg	Val	Glu	Trp	Leu	Arg	Lys	Lys	Leu	Gln	Asp	Val	His	Asn	Phe	Val	Ala
AGA	GTT	GAA	TGG	TTG	AGA	AAG	AAG	CTG	CAG	GAC	GTT	CAC	AAC	TTC	GTT	GCT
TCT	CAA	CTT	ACC	AAC	TCT	TTC	<u>GAC</u>	<u>GTC</u>	CTG	CAA	GTG	TTG	AAG	CAA	CGA	

Pst I

37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53
Leu	Gly	Ala	Pro	Leu	Ala	Pro	Arg	Asp	Ala	Gly	Ser	Gln	Arg	Pro	Arg	Lys
TTG	GGA	GCT	CCA	TTG	GCT	CCA	AGA	GAC	GCT	GGT	TCT	CAA	AGA	CCA	AGA	AAG
AAC	CCT	CGA	GGT	AAC	CGA	GGT	TCT	GTC	CGA	CCA	AGA	GTT	TCT	GGT	TCT	TTC
54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70
Lys	Glu	Asp	Asn	Val	Leu	Val	Glu	Ser	His	Glu	Lys	Ser	Leu	Gly	Glu	Ala
AAG	GAA	GAC	AAC	GTT	TTG	GTT	GAA	TCT	CAC	GAA	AAG	TCT	TTG	GGT	GAA	GCT
TTC	CTT	CTG	TTG	CAA	AAC	CAA	CTT	AGA	GTG	CTT	TTC	AGA	AAC	CCA	CTT	CGT
71	72	73	74	75	76	77	78	79	80	81	82	83	84			
Asp	Lys	Ala	Asp	Val	Asn	Val	Leu	Thr	Lys	Ala	Lys	Ser	Gln	term		
GAC	AAG	GCT	GAC	GTT	AAC	GTG	TTA	ACT	AAG	GCT	AAA	TCG	CAA	TAA-		
CTG	TTC	GCA	CTG	CAA	TTG	CAC	AAT	TGA	TTC	CGA	TTT	AGC	GTT	ATT-		

ATA TCT TCA AGC TTG GCA.....
TCT AGA ACT TCG AAC CGT.....

Bgl II Hind III

NUCLEOTIDE SEQUENCE ENCODING PTH IN PLASMID pPTH-84

FIG. I

SUBSTITUTE SHEET

2/14

A

1 2 3 4 5
Ser Val Ser Glu Ile

PI

5'-AA TTC TGT AAG GGA TCC AAG AAG AGA TCG GTT TCT GAG ATC
G ACA TTC CCT AGG TTC TTC TCT AGC CAA AGA CTC TAG

PVIII

6 7 8 9 10 11 12 13 14 15 16 17 18 19
Gln Leu Met His Asn Leu Gly Lys His Leu Asn Ser Met Glu

PII

CAA TTG ATG CAT AAC TTG GGT AAG CAC TTG AAC TCT ATG GAA
GTT AAC TAC GTA TTG AAC CCA TTC GTG AAC TTG AGA TAC CTT

PVII

20 21 22 23 24 25 26 27 28 29 30 31 32 33
Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His Asn

PIII

AGA GTT GAA TGG TTG AGA AAG AAG CTG CAG GAC GTT CAC AAC
TCT CAA CTT ACC AAC TCT TTC TTC GAC GTC CTG CAA GTG TTG

PVI

34 35 36 37 38 39
Phe Val Ala Leu Gly Ala

TTC GTT GCT TTG GGA GCT CCA TA
AAG ATT CGA AAC CCT CGA GGT ATT CGA-5'
SstI HindIII

TER

DESIGN OF DNA SEQUENCES ENCODING PTH AND ANALOGS.
ENDS OF OLIGONUCLEOTIDES ARE INDICATED BY ARROWS.
BASE-MISMATCHING REGIONS FOR GENERATING ANALOGS ARE
CONTAINED IN BOXES.

(A) OLIGONUCLEOTIDES PI-PVIII CODING FOR PTH
(POSITIONS 1-40) FOR THE CONSTRUCTION OF
PLASMIDS pPTH-34 AND pPTH-40.

FIG. 2

..... CONTINUED

SUBSTITUTE SHEET

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B

40 41 42 43 44 45 46 47 48 49 50
 Pro Leu Ala Pro Arg Asp Ala Gly Ser Gln Arg
SstI PIX
 CCA TTG GCT CCA AGA GAC GCT GGT TCT CAA AGA
 3'-T CGA GGT AAC CGA GGT TCT CTG CGA CCA AGA GTT TCT
 PXIV

51 52 53 54 55 56 57 58 59 60 61 62 63
 Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser His
 PX
 CCA AGA AAG AAG GAA GAC AAC GTT TTG GTT GAA TCT CAC
 GGT TCT TTC CTT CTG TTG CAA AAC CAA CTT AGA GTG
 PXV

64 65 66 67 68 69 70 71 72 73 74 75 76
 Glu Lys Ser Leu Gly Glu Ala Asp Lys Ala Asp Val Asn
 PXI
 GAA AAG TCT TTG GGT GAA GCT GAC AAG GCT GAC GTT AAC
 CTT TTC AGA AAC CCA CTT CGA CTG TTC CGA CTG CAA TTG
 PXIV

77 78 79 80 81 82 83 84
 Val Leu Thr Lys Ala Lys Ser Gln Ter
 PXII
 GTG TTA ACT AAG GCT AAA TCG CAA TAA AGA TCT TGA
 CAC AAT TGA TTC CGA TTT AGC GTT ACA TCT AGA ACT TCG A-5'
 PXIII CYS BgIII HindIII

(B) OLIGONUCLEOTIDES PIX-PXVI CODING FOR PTH
 (POSITIONS 38-84) FOR THE CONSTRUCTION OF
 PLASMIDS pPTH-84 AND pPTH-87.

FIG. 2

(CONTINUED)

SUBSTITUTE SHEET

4/14

1 2 3 4
fMet Ser Val Ser Glu
 P1AA

5' COL-1
ACAA TTT CAC ACA GG AAA CA G | CT ATG TCA GTA TCA GAA-
 [TGT CC TTT GT C GA TAC AGT CAT AGT CTT-
 P8AA

RBS

5 6 7 8 9 10 11 12 13 14 15 16 17
Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn Ser
 P2B

ATA CAA TTA ATG CAT AAT TTA GGT AA G CAC TTG AAC TCT-
TAT [GTT AAT TAC GTA TTA AAT CCA TT [C GTG AAC TTG AGA-
 P7B

18 19 20 21 22 23 24 25 26 27 28 29
Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln
 P3

ATG GAA AGA GTT GAA TGG TTG AGA AAG AAG CTG CA
TAC CTT TCT CAA CTT ACC AAC TCT TTC TTC G
 Pst I
 P6

OLIGONUCLEOTIDES COL-1, P1AA, P2B, P3, P6, P7B
AND P8AA FOR THE CONSTRUCTION OF ADENINE-RICH
CODING SEQUENCE OF PTH-(1-28) IN PLASMID pPTH-AA.

FIG. 3

SUBSTITUTE SHEET

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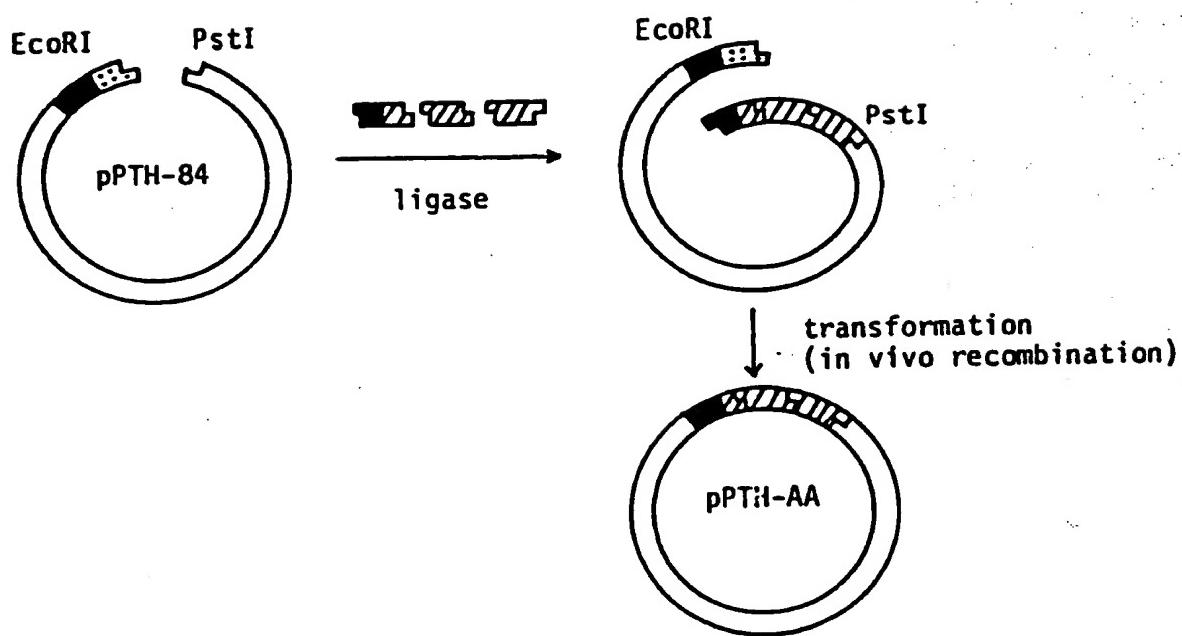
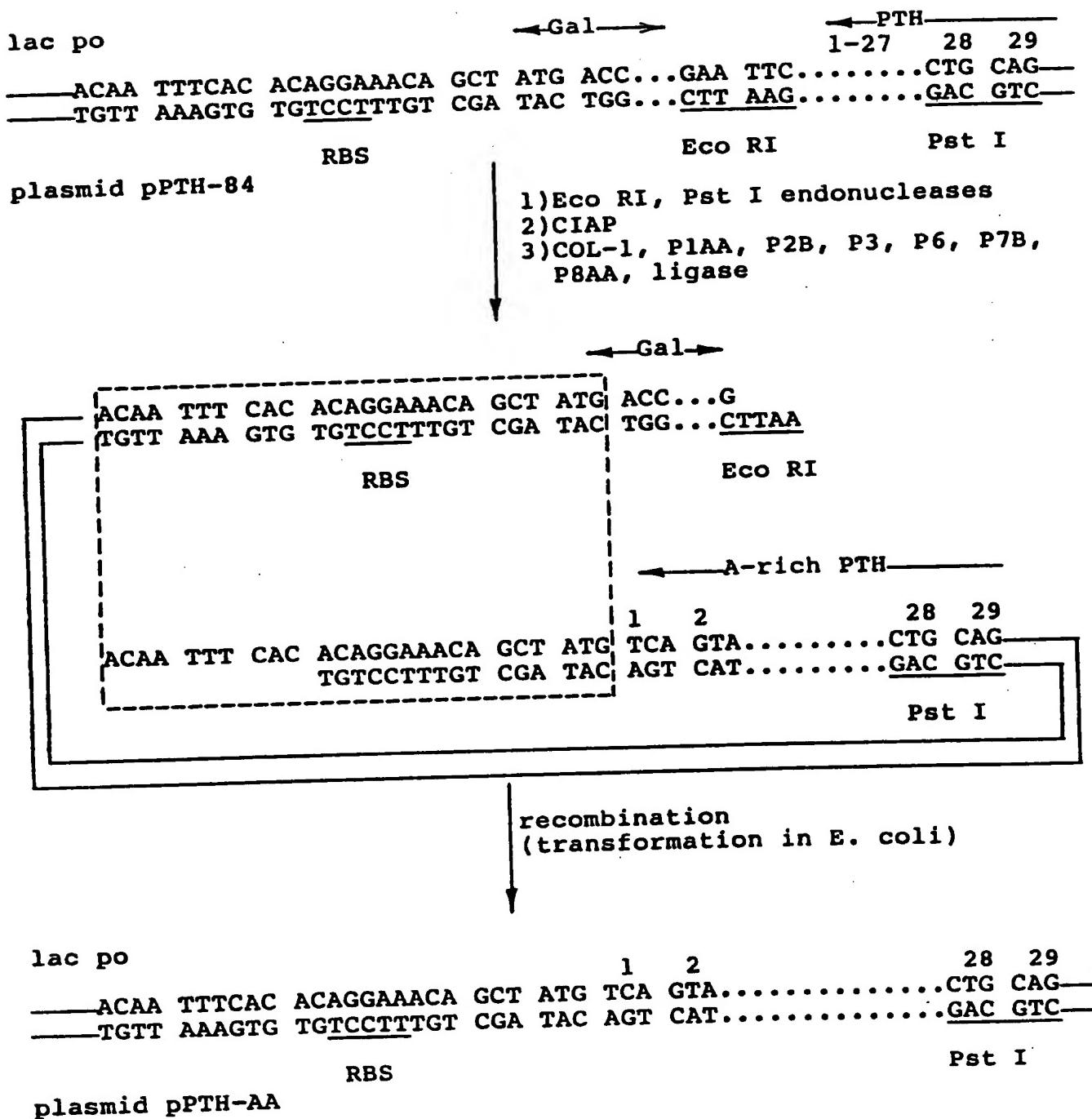


FIG. 4

SUBSTITUTE SHEET

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SYNTHESIS OF PLASMID pPTH-AA CONTAINING AN A-RICH
PTH-CODING SEQUENCE

FIG. 5
SUBSTITUTE SHEET

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28 29 30 31 32 33 34 35 36 37 38 39 40 41
 Leu Gln Asp Val His Asn Phe Val Ala Leu Gly Ala Pro Leu
P103b
 G GAC GTT CAC AAT TTC GTT GCG CTG GGC GCT CCG CT G-
AC GTC CTG CAA GTG TTA AAG CAA CGC GAC CCG CGA GGC GA C-
P204a

Pst I

42 43 44 45 46 47 48 49 50 51 52 53 54 55
 Ala Pro Arg Asp Ala Gly Ser Gln Arg Pro Arg Lys Lys Glu
P104
 GCA CCG CGT GAC GCT GGT TCT CAA CGC CCG CGT AAG AAA GAA-
CGT GGC GCA CTG CGA CCA AGA GTT GCG GGC GCA TTC TTT CTT-
P203

56 57 58 59 60 61 62 63 64 65 66 67 68 69 70
 Asp Asn Val Leu Val Glu Ser His Glu Lys Ser Leu Gly Glu Ala
P105
GAT AAC GTT CTG GTT GAA TCC CAT GAG AAA TCT CTG GGC GAA GCC-
CTA TTG CAA GAC CAA CTT AGG GTA CTC TTT AGA GAC CCG CTT CGG-
P202

71 72 73 74 75 76 77 78 79 80 81 82 83 84
 Asp Lys Ala Asp Val Asn Val Leu Thr Lys Ala Lys Ser Gln Term
P106
GAC AAA GCG GAT GTG AAC GTT CTG ACC AAA GCT AAA TCC CAG TAA-
CTG TTT CGC CTA CAC TTG CAA GAC TGG TTT CGA TTT AGG GCT ATT-
P201

-AGA TCT TGA
 -TCT AGA ACT TCG A

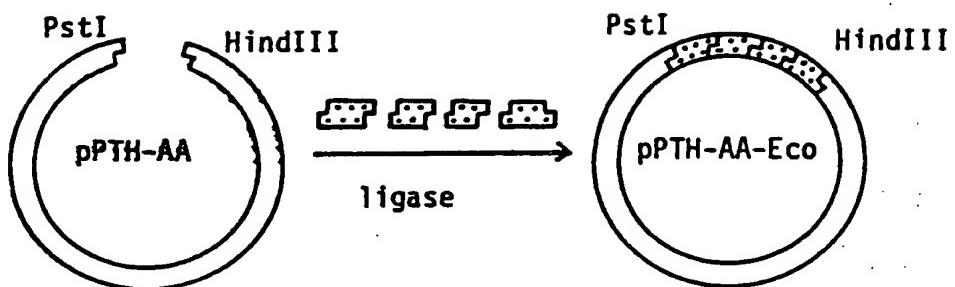
Hind III

OLIGONUCLEOTIDES P103b, P104, P105, P201, P202, P203
 and P204a FOR THE CONSTRUCTION OF NUCLEOTIDE SEQUENCE
 ENCODING PTH-(29-84) with E. COLI-FAVORED CODONS.

FIG.6

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DIAGRAMMATIC SCHEME FOR THE CONSTRUCTION OF pPTH-AA-Eco.
OVERLAPPING OLIGONUCLEOTIDE DUPLEXES P103b, P104, P105,
P106, P201, P202, P203, AND P204a (STIPPLED), WHICH
CONSTITUTED THE CODING SEQUENCE FOR PTH-(29-84) WERE
LIGATED TO THE PstI/HindIII-LINEARIZED PLASMID TO YIELD
A NEW PLASMID pPTH-AA-Eco.

FIG. 7

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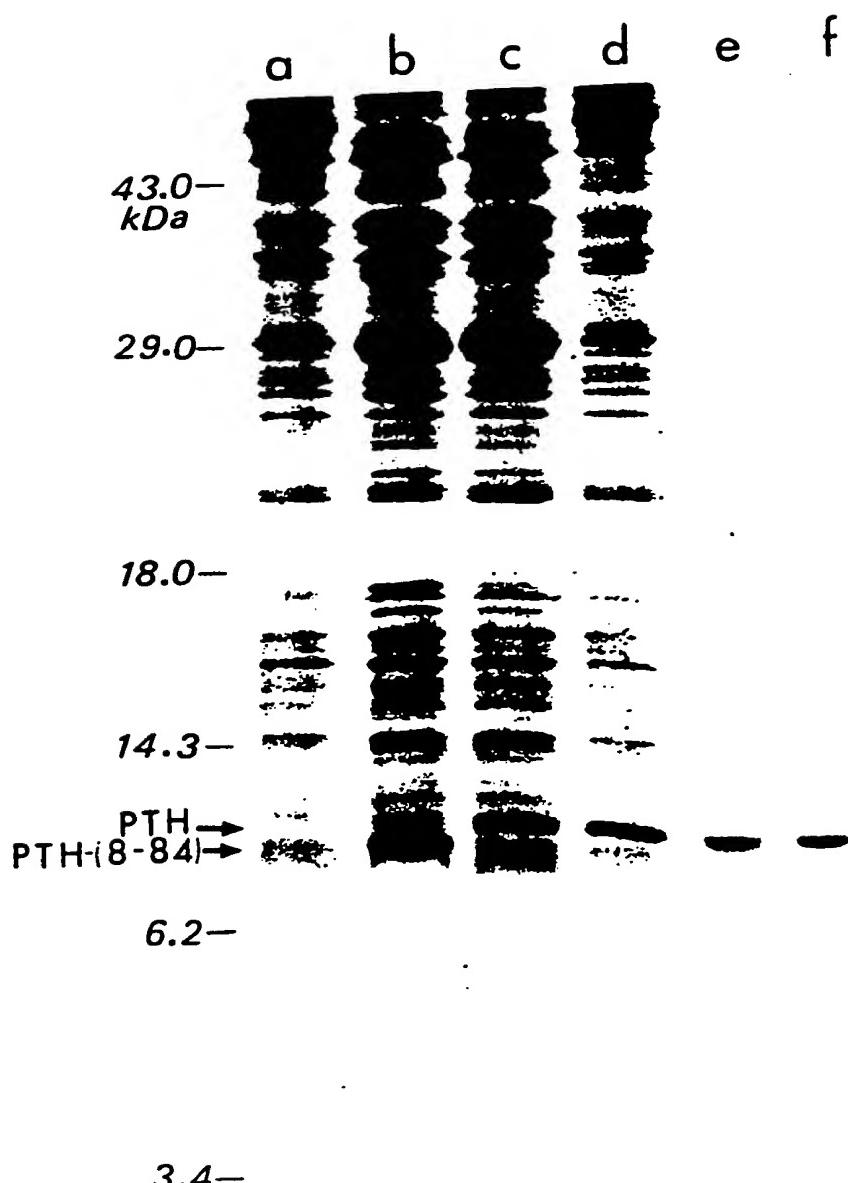
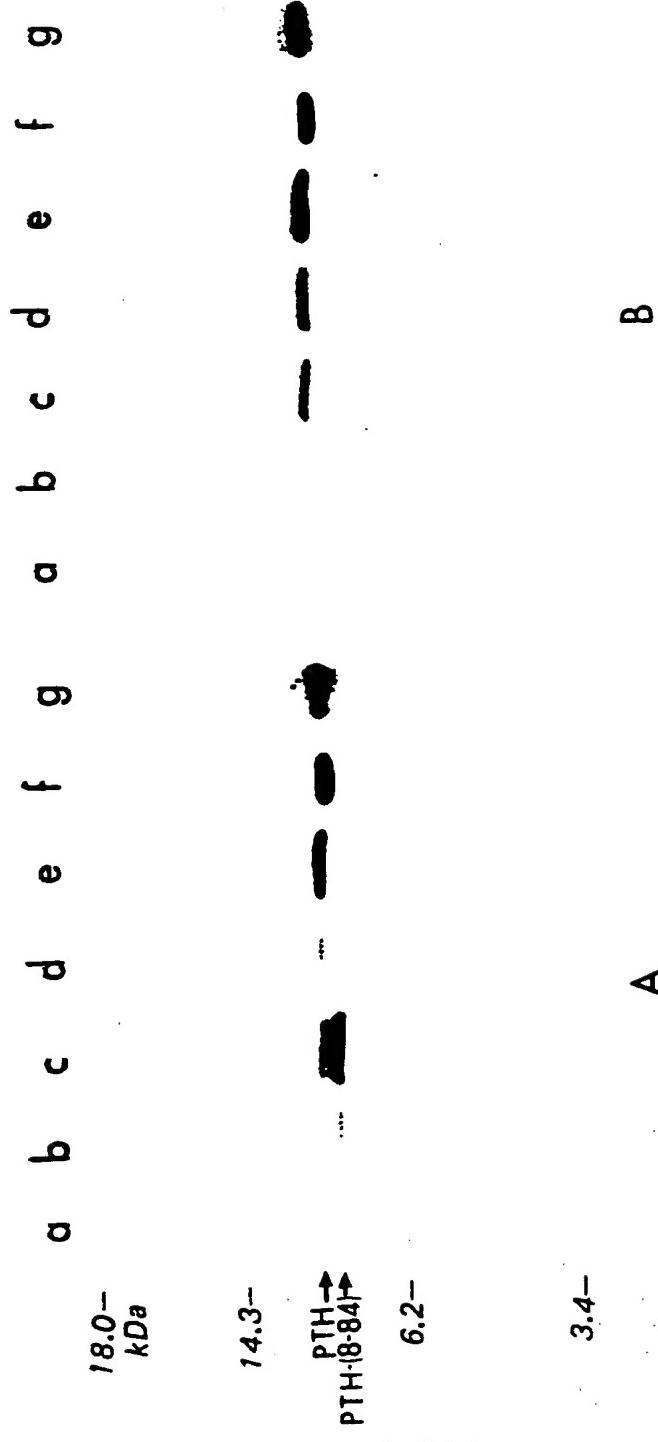


FIG. 8

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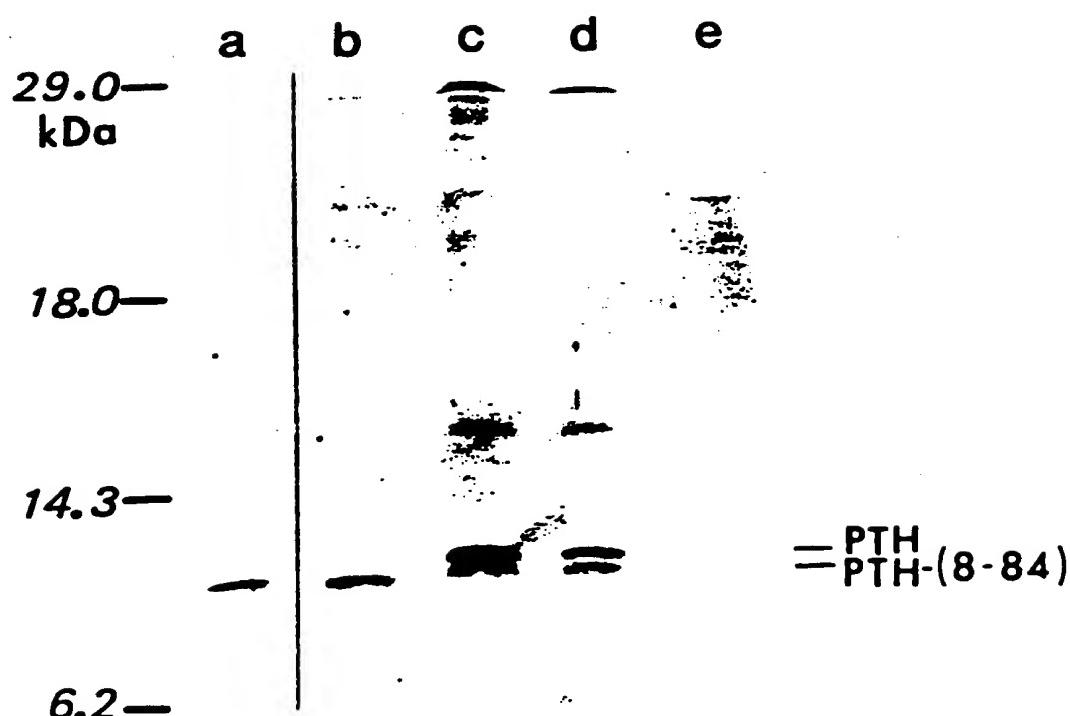


FIG. 10

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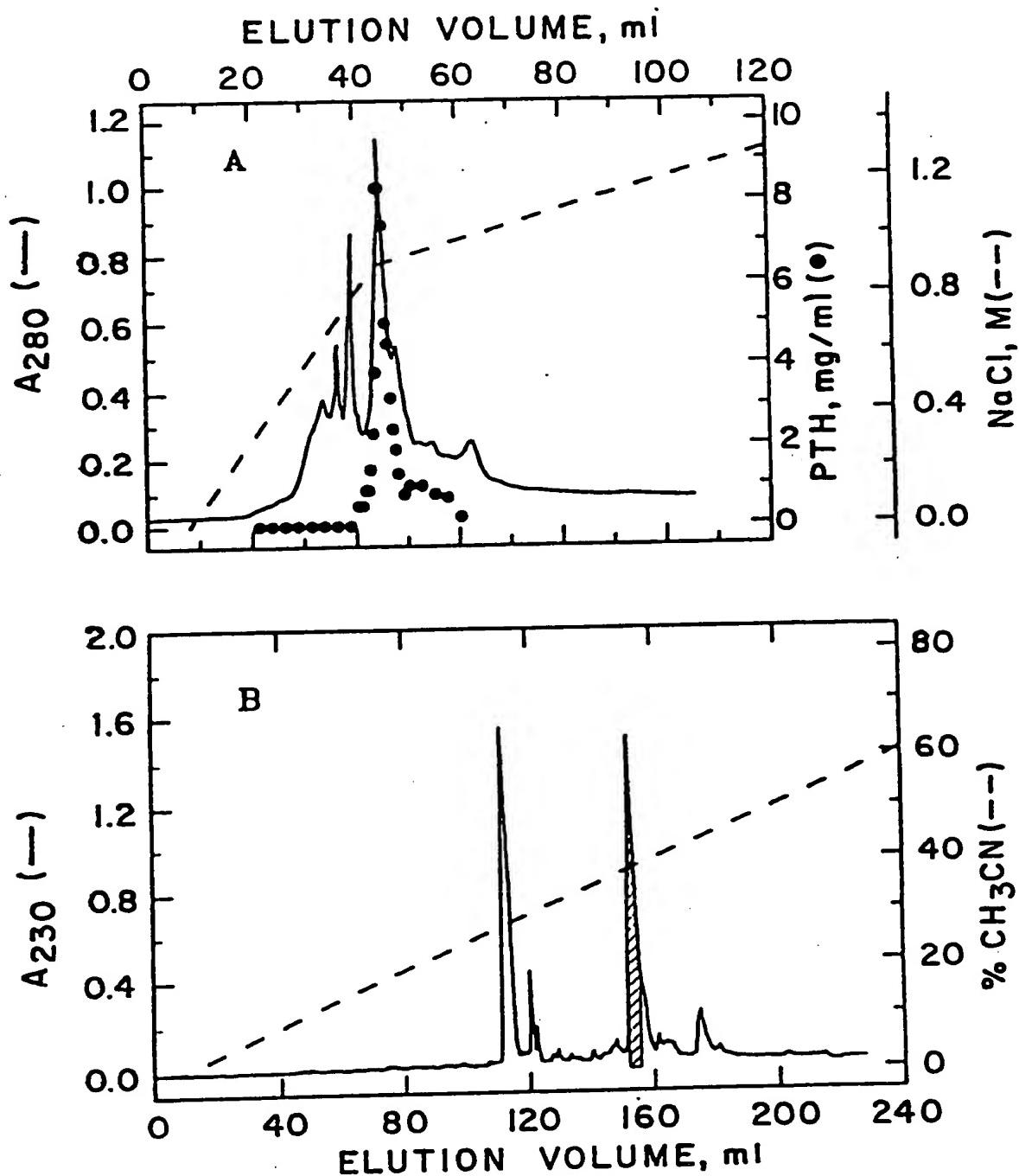


FIG. II

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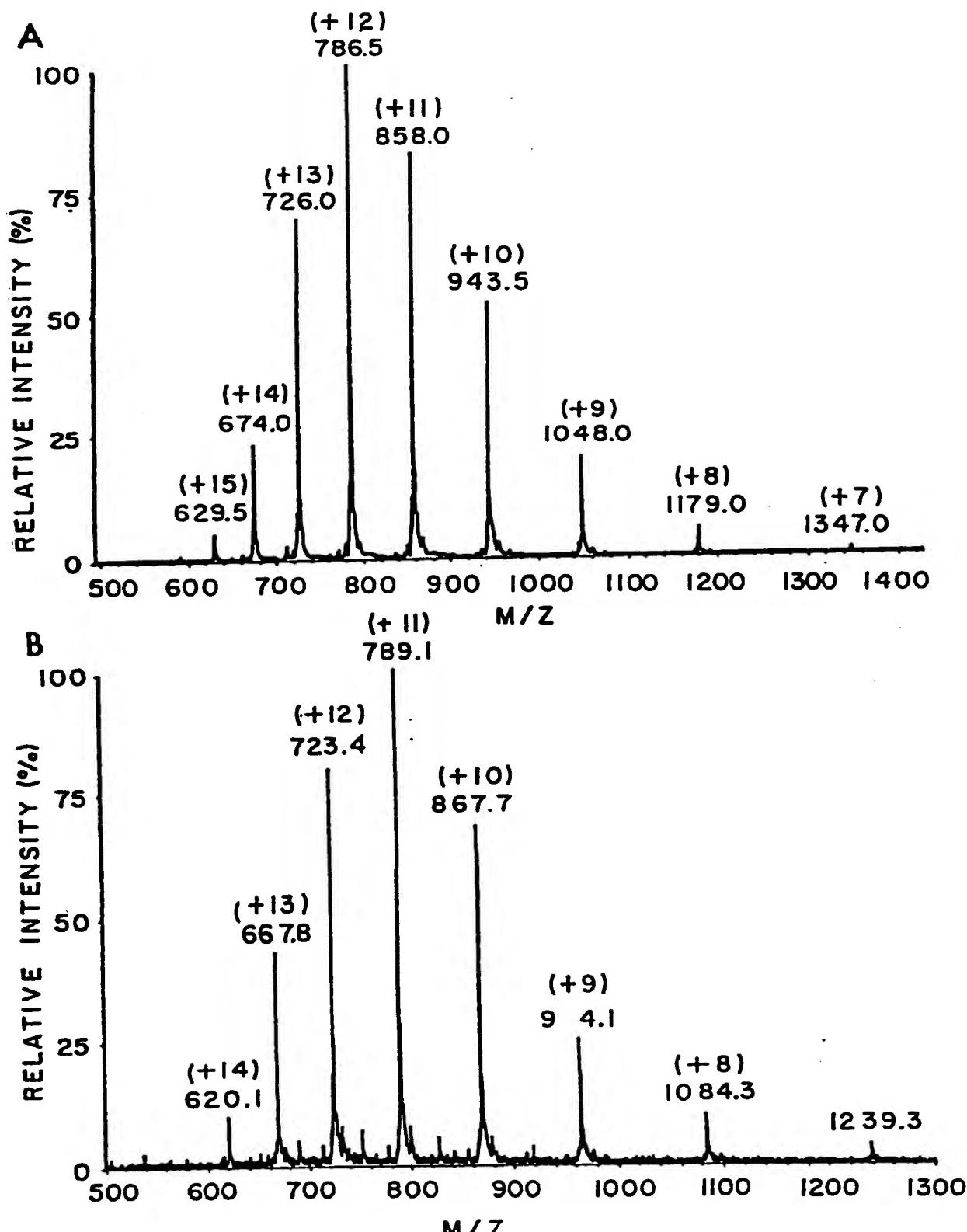
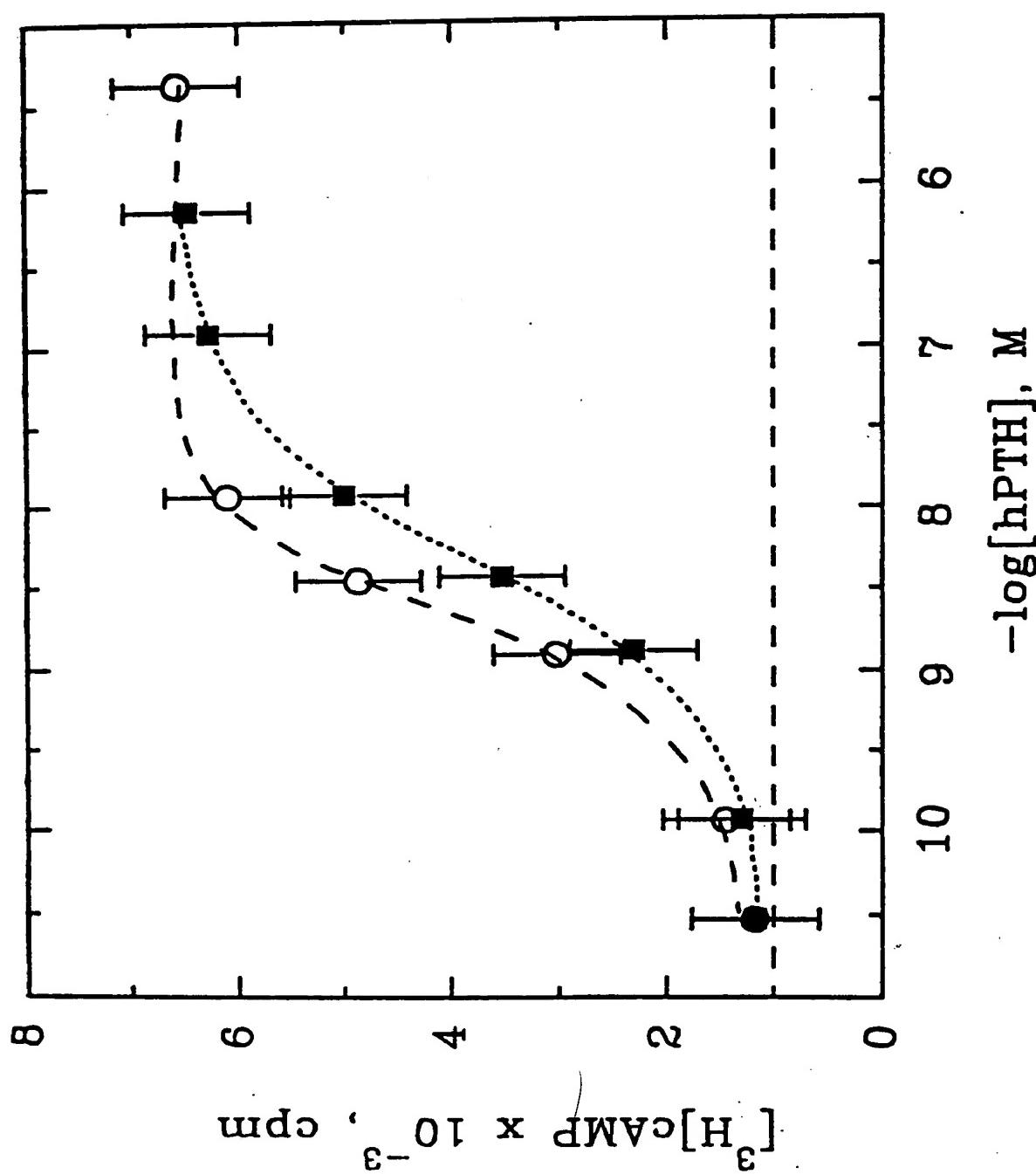


FIG. 12

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FIG.13



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INTERNATIONAL SEARCH REPORT

International Application No PCT/CA 90/00335

I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all) *

According to International Patent Classification (IPC) or to both National Classification and IPC

IPC⁵: C 12 N 15/67, C 12 N 1/21 // (C 12 N 1/21, C 12 R 1:19) C 12 N 15/16,

II. FIELDS SEARCHED

Minimum Documentation Searched ?

Classification System	Classification Symbols
IPC ⁵	C 07 K, C 12 N

Documentation Searched other than Minimum Documentation
to the Extent that such Documents are Included in the Fields Searched *

III. DOCUMENTS CONSIDERED TO BE RELEVANT*

Category *	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
A	European Congress of Biotechnology, volume 3, 1984, E. Breyel et al.: "Synthesis of mature human parathyroid hormone in Escherichia coli", pages 363-369 see the whole document cited in the application ---	1
A	WO, A, 88/03165 (G. MODIANO et al.) 5 May 1988 see the whole document ---	1
A	Biochimica et Biophysica Acta, volume 950, 1988, Elsevier, (Amsterdam, NL), G. Morelle et al: "Increased synthesis of human parathyroid hormone in Escherichia coli through alterations of the 5' untranslated region", pages 459-462 see the whole document cited in the application -----	1

- * Special categories of cited documents: 10
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- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search

14th January 1991

Date of Mailing of this International Search Report

- 1. 02. 91

International Searching Authority

EUROPEAN PATENT OFFICE

Signature of Authorized Officer

M. PEIS

1. 02. 91

**ANNEX TO THE INTERNATIONAL SEARCH REPORT
ON INTERNATIONAL PATENT APPLICATION NO.**

CA 9000335
SA 40446

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report.
The members are as contained in the European Patent Office EDP file on 28/01/91.
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Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO-A- 8803165	05-05-88	AU-A-	8104887	25-05-88